



SEQUENCE LISTING

(1)

GENERAL INFORMATION:

- (i) APPLICANT: FALCO, SAVERIO CARL
ALLEN, STEPHEN M.
RAFALSKI, J. ANTONI
HITZ, WILLIAM D.
KINNEY, ANTHONY J.
ABELL, LYNNE N.
THORPE, CATHERINE J.
- (ii) TITLE OF INVENTION: PLANT AMINO ACID BIOSYNTHETIC ENZYMES
- (iii) NUMBER OF SEQUENCES: 43
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
 - (B) STREET: 1007 MARKET STREET
 - (C) CITY: WILMINGTON
 - (D) STATE: DELAWARE
 - (E) COUNTRY: USA
 - (F) ZIP: 19898
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: DISKETTE, 3.50 INCH
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
 - (D) SOFTWARE: MICROSOFT WORD VERSION 7.0A
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US/10/734,698
 - (B) FILING DATE: 12-Dec-2003
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/048,771
 - (B) FILING DATE: 6-Jun-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: MAJARIAN, WILLIAM R.
 - (B) REGISTRATION NUMBER: 41,173
 - (C) REFERENCE/DOCKET NUMBER: BB-1087
 - (G) TELEPHONE: 302-992-4926
 - (H) TELEFAX: 302-773-0164

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 908 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: cs11n.pk0042.a3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
ACGCGGGACA GATAAGTGGC ATGGACGAGC CGCTGGAGAT CCCTGTGCTG AACGACCTCA      60
CCATGGTTCT GGGCTCCATA GCGCAGTCGA GAGCAACCGG CGTGGTGGTC GACTTCAGCG      120
AGCCTTCAGC TGTTTACGAC AATGTCAAGC AGGCAGCGGC GTTTGGTCTG AGCAGCGTCG      180
TCTACGTTCC GAAAATCGAG CTAGAGACAG TGA CTGAACT GTCAGCGTTC TGCGAGAAGG      240
CAAGCGGCTG CTTGGTTGCG CCAACGCTGT CGATTGGGTC CGTGCTCCTT CAGCAAGCGG      300
CTATACAGGC CTCGTTCCAC TACAGCAACG TTGAGATTGT GGAATCGAGA CCAAACCCAT      360
CGGATCTTCC ATCGCAAGAT GCAATCCAGA TTGCAAACAA CATATCAGAC CTTGGTCAGA      420
TATACAACAG GGAAGATATG GATTCCAGCA GTCCAGCCAG AGGCCAGCTG CTCGGGGAAG      480
ACGGAGTGCG CGTGCACAGC ATGGTTCTCC CTGGTCTCGT CTCCAGCACG TCGATCAACT      540
TCTCTGGCCC AGGAGAGATG TACACCTTAC GGCATGACGT TGCGAATGTT CAGTGCCTGA      600
TGCCAGGACT GATCCTGGCG ATACGGAAGG TGGTGCGGTT CAAGAACTTG ATTTATGGGC      660
TAGAGAAGTT CTTGTAGTGA ACAACAAACA ACCAATGCAA AACATCGACA GGCAACAGGC      720
AAGGCAGATA TCATCTGACG TCGCAACAAC CAAAACGACA GAGATTTGGA AAATAAAGGC      780
TGCACAGAAG ACGTCTGGGG TTTTGTGTGC ACCAGGCTGC GCAGAGAACG TCTGTCATTT      840
TGTGTGCACC ACTACGGCAC TACCTGCTGA GCGCGATTTT TATAAAAAG GCATGGGAGG      900
GAGATCAT                                         908
```

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: cs11n.pk0042.a3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Ala Gly Gln Ile Ser Gly Met Asp Glu Pro Leu Glu Ile Pro Val Leu
1           5           10           15
Asn Asp Leu Thr Met Val Leu Gly Ser Ile Ala Gln Ser Arg Ala Thr
20           25           30
Gly Val Val Val Asp Phe Ser Glu Pro Ser Ala Val Tyr Asp Asn Val
35           40           45
```

Lys Gln Ala Ala Ala Phe Gly Leu Ser Ser Val Val Tyr Val Pro Lys
 50 55 60
 Ile Glu Leu Glu Thr Val Thr Glu Leu Ser Ala Phe Cys Glu Lys Ala
 65 70 75 80
 Ser Gly Cys Leu Val Ala Pro Thr Leu Ser Ile Gly Ser Val Leu Leu
 85 90 95
 Gln Gln Ala Ala Ile Gln Ala Ser Phe His Tyr Ser Asn Val Glu Ile
 100 105 110
 Val Glu Ser Arg Pro Asn Pro Ser Asp Leu Pro Ser Gln Asp Ala Ile
 115 120 125
 Gln Ile Ala Asn Asn Ile Ser Asp Leu Gly Gln Ile Tyr Asn Arg Glu
 130 135 140
 Asp Met Asp Ser Ser Ser Pro Ala Arg Gly Gln Leu Leu Gly Glu Asp
 145 150 155 160
 Gly Val Arg Val His Ser Met Val Leu Pro Gly Leu Val Ser Ser Thr
 165 170 175
 Ser Ile Asn Phe Ser Gly Pro Gly Glu Met Tyr Thr Leu Arg His Asp
 180 185 190
 Val Ala Asn Val Gln Cys Leu Met Pro Gly Leu Ile Leu Ala Ile Arg
 195 200 205
 Lys Val Val Arg Phe Lys Asn Leu Ile Tyr Gly Leu Glu Lys Phe Leu
 210 215 220

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: rls2.pk0017.d3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGATTGGCA GGAGAAATGC AGCAAAGGTC CTCTGCTCAA CGCAGATGCC GCCATCTCAG	60
AGCACAATCA AGGTTGTTAT CATTGGGGCG ACAAAGAGA TTGGAAGAAC GGCAATAGCG	120
GCAGTAAGTA AAGCAAGGGG AATGGAGCTT GCAGGGGCCA TAGATTCTCA GTGTATAGGC	180
CTAGATGCAG GAGAGATAAG TGGCATGGGA AGAACCTGG AAATTCGGT GCTCAATGAT	240
CTCACAATGG TTCTGGGCTC AATTGCACAA ACCAGAGCAA CTGGAGTGGT GGTGATTTT	300
AGTGAACCTT CAACTGTTTA TGATAATGTC AACAGGCA	339

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: rls2.pk0017.d3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Ile Gly Arg Arg Asn Ala Ala Lys Val Leu Cys Ser Thr Gln Met
1 5 10 15
Pro Pro Ser Gln Ser Thr Ile Lys Val Val Ile Ile Gly Ala Thr Lys
20 25 30
Glu Ile Gly Arg Thr Ala Ile Ala Ala Val Ser Lys Ala Arg Gly Met
35 40 45
Glu Leu Ala Gly Ala Ile Asp Ser Gln Cys Ile Gly Leu Asp Ala Gly
50 55 60
Glu Ile Ser Gly Met Gly Arg Thr Leu Glu Ile Pro Val Leu Asn Asp
65 70 75 80
Leu Thr Met Val Leu Gly Ser Ile Ala Gln Thr Arg Ala Thr Gly Val
85 90 95
Val Val Asp Phe Ser Glu Pro Ser Thr Val Tyr Asp Asn Val Lys Gln
100 105 110
Ala

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Synechocystus sp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Asn Gln Asp Leu Ile Pro Val Val Val Asn Gly Ala Ala Gly
1 5 10 15
Lys Met Gly Arg Glu Val Ile Lys Ala Val Ala Gln Ala Pro Asp Leu
20 25 30

Gln Leu Val Gly Ala Val Asp His Asn Pro Ser Leu Gln Gly Gln Asp
 35 40 45
 Ile Gly Glu Val Val Gly Ile Ala Pro Leu Glu Val Pro Val Leu Ala
 50 55 60
 Asp Leu Gln Ser Val Leu Val Leu Ala Thr Gln Glu Lys Ile Gln Gly
 65 70 75 80
 Val Met Val Asp Phe Thr His Pro Ser Gly Val Tyr Asp Asn Val Arg
 85 90 95
 Ser Ala Ile Ala Tyr Gly Val Arg Pro Val Val Gly Thr Thr Gly Leu
 100 105 110
 Ser Glu Gln Gln Ile Gln Asp Leu Gly Asp Phe Ala Glu Lys Ala Ser
 115 120 125
 Thr Gly Cys Leu Ile Ala Pro Asn Phe Ala Ile Gly Val Leu Leu Met
 130 135 140
 Gln Gln Ala Ala Val Gln Ala Cys Gln Tyr Phe Asp His Val Glu Ile
 145 150 155 160
 Ile Glu Leu His His Asn Gln Lys Ala Asp Ala Pro Ser Gly Thr Ala
 165 170 175
 Ile Lys Thr Ala Gln Met Leu Ala Glu Met Gly Lys Thr Phe Asn Pro
 180 185 190
 Pro Ala Val Glu Glu Lys Glu Thr Ile Ala Gly Ala Lys Gly Gly Leu
 195 200 205
 Gly Pro Gly Gln Ile Pro Ile His Ser Ile Arg Leu Pro Gly Leu Ile
 210 215 220
 Ala His Gln Glu Val Leu Phe Gly Ser Pro Gly Gln Leu Tyr Thr Ile
 225 230 235 240
 Arg His Asp Thr Thr Asp Arg Ala Cys Tyr Met Pro Gly Val Leu Leu
 245 250 255
 Gly Ile Arg Lys Val Val Glu Leu Lys Gly Leu Val Tyr Gly Leu Glu
 260 265 270
 Lys Leu Leu
 275

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1012 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: chp2.pk0008.h4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
TATTGCCAGA GATGTGTGGT AATGGAGTCC GTTGCTTCGC TCGGTTTATA GCCGAGATTG      60
AAAATCTGCA GGGGACAAAT AGATTCACTA TTCATACTGG TGCTGGAAAG ATCGTTCCTG      120
AAATACAAAG TGATGGGCAG GTAAAGGTTG ATATGGGCGA GCCTATCCTT TCTGGACTAG      180
ACATCCCCAC AAAACTGCTA GCTACCAAGA ACAAAGCTGT TGTTCAAGCT GAATTGGCAG      240
TTGAGGGCTT AACATGGCAT GTCACATGTG TTAGCATGGG AAACCCTCAC TGTGTCACAT      300
TTGGTGCAAA TGAGTTAAAG GTATTGCAGG TCGACGATTT AAAACTTAGC GAAATTGGGC      360
CTAAATTTGA GCATCATGAA ATGTTTCCTG CTCGCACAAA CACAGAATTC GTACAGGTTT      420
TGTCTCGCTC ACACCTCAA A TGCGGGTCT GGAACGTGG TGCTGGAGCA ACTCTTGCCT      480
GTGGTACTGG TGCTTGTGCA GTGGTTGTTG CAGCTGTTCT TGAGGGTCGA GCTGAGCGGA      540
AATGTGTAGT TGATTTGCCT GGCGGGCCAT TGGAAATTGA GTGGAGGGAG GATGACAATC      600
ATGTTTACAT GACTGGTCCT GCAGAGGTCG TCTTTTATGG ATCTGTTGTT CACTAGGTAC      660
TGGGGACCAA GATAGAAGGG TTGGCTGCCA CTCAGAGCTT GTGAGATTGG TTATAGTATC      720
CATGAAACAG AGTGTTCCTG TACCAGTACA CTTGTTCAGA TATTCTTAAT TATGATTGCT      780
TGATTTGGGT AGCMGTAGAG GCTTCCTTTT GAAGCATTCT AGTGTTTCMCC TTTTGTACTC      840
CTTTAGTTTG TCAGGTTTGA ACACTACATG GGTAACATGT CYTTCCCACC ATTTTCYGTT      900
TCTTTTCTTT GTAAGTGAAC GCCAATGCAG TTTTAGTATT GTTTTCTATA GATTGTCTT      960
GATGCACTGG GCTTACTACT TATTTTCTGG TATGAATGCT GCCTATTTCC TG      1012
```

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: chp2.pk0008.h4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Leu Pro Glu Met Cys Gly Asn Gly Val Arg Cys Phe Ala Arg Phe Ile
1           5           10           15
Ala Glu Ile Glu Asn Leu Gln Gly Thr Asn Arg Phe Thr Ile His Thr
20           25           30
Gly Ala Gly Lys Ile Val Pro Glu Ile Gln Ser Asp Gly Gln Val Lys
35           40           45
```

Val	Asp	Met	Gly	Glu	Pro	Ile	Leu	Ser	Gly	Leu	Asp	Ile	Pro	Thr	Lys	
50						55					60					
Leu	Leu	Ala	Thr	Lys	Asn	Lys	Ala	Val	Val	Gln	Ala	Glu	Leu	Ala	Val	
65					70					75					80	
Glu	Gly	Leu	Thr	Trp	His	Val	Thr	Cys	Val	Ser	Met	Gly	Asn	Pro	His	
				85					90					95		
Cys	Val	Thr	Phe	Gly	Ala	Asn	Glu	Leu	Lys	Val	Leu	Gln	Val	Asp	Asp	
			100					105					110			
Leu	Lys	Leu	Ser	Glu	Ile	Gly	Pro	Lys	Phe	Glu	His	His	Glu	Met	Phe	
		115					120					125				
Pro	Ala	Arg	Thr	Asn	Thr	Glu	Phe	Val	Gln	Val	Leu	Ser	Arg	Ser	His	
		130				135						140				
Leu	Lys	Met	Arg	Val	Trp	Glu	Arg	Gly	Ala	Gly	Ala	Thr	Leu	Ala	Cys	
145					150					155					160	
Gly	Thr	Gly	Ala	Cys	Ala	Val	Val	Val	Ala	Ala	Val	Leu	Glu	Gly	Arg	
				165					170					175		
Ala	Glu	Arg	Lys	Cys	Val	Val	Asp	Leu	Pro	Gly	Gly	Pro	Leu	Glu	Ile	
			180					185						190		
Glu	Trp	Arg	Glu	Asp	Asp	Asn	His	Val	Tyr	Met	Thr	Gly	Pro	Ala	Glu	
		195					200					205				
Val	Val	Phe	Tyr	Gly	Ser	Val	Val	His								
		210				215										

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: rls48.pk0036.h10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGTATCCGGC GCCGACGGTG TGATCTTCGT CATGCCGGGG GTCAATGGCG CGGACTACAC	60
CATGAGGATC TTCAACTCGG ACGGCAGTGA GCCGGAGATG TGTGGCAATG GAGTCCGTTG	120
CTTTGCCCCG TTTATAGCTG AGCTTGAAAA CCTACAGGGA ACACATAGCT TCAAAATTCA	180
CACTGGCGCT GGGCTAATCA TTCCTGAAAT ACAAATGAT GGCAAGGTAA AGGTTGATAT	240
GGGCCAGCCC ATTCTCTCTG GACCAGATAT TCCAACAAAA CTGCCATCCA CCAAGAATGA	300
AGCCGTTGTC CAAGCTGATT TGGGCAGTTG ATGGCTCAAC ATGGCAAGTA ACCTGTGTTA	360

GCATGGGCAA TCCACATTGT GTCACATTTG GCACAAAGGA GCTCAAGGTT TTGCATGTTG 420
 ATGATTAAAG CTTAATGATA TTGGGGCCTA AATTCAGCAT CATGAAATGT TCCTGCCCCA 480
 C 481

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: rls48.pk0036.h10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Ser Gly Ala Asp Gly Val Ile Phe Val Met Pro Gly Val Asn Gly
 1 5 10 15
 Ala Asp Tyr Thr Met Arg Ile Phe Asn Ser Asp Gly Ser Glu Pro Glu
 20 25 30
 Met Cys Gly Asn Gly Val Arg Cys Phe Ala Arg Phe Ile Ala Glu Leu
 35 40 45
 Glu Asn Leu Gln Gly Thr His Ser Phe Lys Ile His Thr Gly Ala Gly
 50 55 60
 Leu Ile Ile Pro Glu Ile Gln Asn Asp Gly Lys Val Lys Val Asp Met
 65 70 75 80
 Gly Gln Pro Ile Leu
 85

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCCCTTATT AAGCAGGGGT TTCGCGGCGC GAGACGGTGA CACTGGCAGA GTGGAATTTC 60
 CGCCGCCATT CGAAGCTACA GCGATGGCCA TAACCGCCAC CATTTCGGTT CCCCTCACAT 120
 CCCCCAGTCG CCGCACTCTC ACCTCCGTCA ATAGCCTCTC TCCCCTTTCT ACCCGATCCA 180
 CTTTGCCCAC ACCGCAACGC ACTTTCAAAT ACCCTAATTC GCGCCTCGTC GTGTCTTCCA 240

TGAGCACCGA AACAGCCGTC AAAACTTCAT CCGCCTCCTT CCTCAACCGC AAGGAGTCCG	300
GCTTCCTCCA TTTGCGCAAG TACCACGGCC TCGGAAACGA CTTGTTTTTG ATTGACAATA	360
GAGACTCCTC CGAGCCCAAG ATCAGTGCTG AGAAAGCGGT GCAACTGTGT GATCGGAACT	420
TCGGCGTTGG AGCTGACGGA GTTATCTTTG TCTTGCCTGG CATCAGTGGC ACCGATTATA	480
CCATGAGGAT TTTTAACTCT GATGGTAGTG AGCCTGAGAT GTGTGGCAAT GGAGTTCGAT	540
GCTTTGCCAA ATTTGTTTCT CAGCTTGAGA ATTTACATGG GAGGCATAGT TTTACCATTC	600
ATACTGGTGC TGGTCTGATT ATTCCTGAAG TCTTGGAGGA TGGAAATGTC AGAGTTGATA	660
TGGGGGAGCC AGTTCTTAAA GCCTTGGATG TGCCTACTAA ATTACCTGCA AATAAGGATA	720
ATGCTGTTGT TAAATCACAG CTAGTTGTAG ATGGAGTTAT TTGGCATGTG ACCTGTGTTA	780
GCATGGGGAA TCCACACTGT GTAACCTTCA GTAGAGAAGG AAGCCAGAAT TTGCTTGTTG	840
ATGAATTGAA GCTAGCAGAA ATTGGGCCAA AATTTGAACA TCATGAGGTG TTCCCTGCAC	900
GAAC TAACAC AGAGTTTGTG CAAGTATTAT CTAACCTCTCA CTTGAAAATG CGTGTTTGGG	960
AGCGGGGAGC AGGAGCAACC CTAGCCTGTG GAACTGGAGC TTGTGCTACT GTTGTTCAG	1020
CAGTTCTTGA GGGTCGTGCT GGGAGGAATT GCACGGTTGA TCTACCTGGA GGGCCTCTTC	1080
AGATTGAGTG GAGGGAGGAA GATAATCATG TTTATATGAC AGGCTCAGCC GATGTAGTTT	1140
ATTATGGTTC TTTGCCCTT TGATATGTTG CCCCATTGT TAAACCCAAT ATGGAATTAG	1200
GAATTGGTGA ATAATATTTG TATGAGAGGT GGACTTTCTG CTTGTTCTTA ATATTTTGCC	1260
ACGTCTTTAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A	1301

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ala	Ile	Thr	Ala	Thr	Ile	Ser	Val	Pro	Leu	Thr	Ser	Pro	Ser	Arg
1			5					10						15	
Arg	Thr	Leu	Thr	Ser	Val	Asn	Ser	Leu	Ser	Pro	Leu	Ser	Thr	Arg	Ser
			20				25						30		
Thr	Leu	Pro	Thr	Pro	Gln	Arg	Thr	Phe	Lys	Tyr	Pro	Asn	Ser	Arg	Leu
		35				40						45			
Val	Val	Ser	Ser	Met	Ser	Thr	Glu	Thr	Ala	Val	Lys	Thr	Ser	Ser	Ala
	50				55					60					

Ser	Phe	Leu	Asn	Arg	Lys	Glu	Ser	Gly	Phe	Leu	His	Phe	Ala	Lys	Tyr	65	70	75	80
His	Gly	Leu	Gly	Asn	Asp	Phe	Val	Leu	Ile	Asp	Asn	Arg	Asp	Ser	Ser	85	90	95	
Glu	Pro	Lys	Ile	Ser	Ala	Glu	Lys	Ala	Val	Gln	Leu	Cys	Asp	Arg	Asn	100	105	110	
Phe	Gly	Val	Gly	Ala	Asp	Gly	Val	Ile	Phe	Val	Leu	Pro	Gly	Ile	Ser	115	120	125	
Gly	Thr	Asp	Tyr	Thr	Met	Arg	Ile	Phe	Asn	Ser	Asp	Gly	Ser	Glu	Pro	130	135	140	
Glu	Met	Cys	Gly	Asn	Gly	Val	Arg	Cys	Phe	Ala	Lys	Phe	Val	Ser	Gln	145	150	155	160
Leu	Glu	Asn	Leu	His	Gly	Arg	His	Ser	Phe	Thr	Ile	His	Thr	Gly	Ala	165	170	175	
Gly	Leu	Ile	Ile	Pro	Glu	Val	Leu	Glu	Asp	Gly	Asn	Val	Arg	Val	Asp	180	185	190	
Met	Gly	Glu	Pro	Val	Leu	Lys	Ala	Leu	Asp	Val	Pro	Thr	Lys	Leu	Pro	195	200	205	
Ala	Asn	Lys	Asp	Asn	Ala	Val	Val	Lys	Ser	Gln	Leu	Val	Val	Asp	Gly	210	215	220	
Val	Ile	Trp	His	Val	Thr	Cys	Val	Ser	Met	Gly	Asn	Pro	His	Cys	Val	225	230	235	240
Thr	Phe	Ser	Arg	Glu	Gly	Ser	Gln	Asn	Leu	Leu	Val	Asp	Glu	Leu	Lys	245	250	255	
Leu	Ala	Glu	Ile	Gly	Pro	Lys	Phe	Glu	His	His	Glu	Val	Phe	Pro	Ala	260	265	270	
Arg	Thr	Asn	Thr	Glu	Phe	Val	Gln	Val	Leu	Ser	Asn	Ser	His	Leu	Lys	275	280	285	
Met	Arg	Val	Trp	Glu	Arg	Gly	Ala	Gly	Ala	Thr	Leu	Ala	Cys	Gly	Thr	290	295	300	
Gly	Ala	Cys	Ala	Thr	Val	Val	Ala	Ala	Val	Leu	Glu	Gly	Arg	Ala	Gly	305	310	315	320
Arg	Asn	Cys	Thr	Val	Asp	Leu	Pro	Gly	Gly	Pro	Leu	Gln	Ile	Glu	Trp	325	330	335	
Arg	Glu	Glu	Asp	Asn	His	Val	Tyr	Met	Thr	Gly	Ser	Ala	Asp	Val	Val	340	345	350	
Tyr	Tyr	Gly	Ser	Leu	Pro	Leu	355												

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 602 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: wlm24.pk0030.g4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

CTCCACCGCC CCCTCCTCGG GCGGTCGCCT CCTCCGTCCG TTCTGTGGGA ATCCGCGCCC      60
CCGCCGCGCC GTCGCCTCGA TGGCCGTGTC CGCTCCCAAG TCGCCAGCCG CCGCCTCGTT      120
CCTCGAGCGC CGCGAGTCCG AGCGCGCGCT CCACTTCGTG AAGTACCAGG GCCTCGGCAA      180
CGACTTCATA ATGGTCGACA ACAGGGATTC GGCCGTACCG AAGGTGACAC CGGAGGAGGC      240
GGCGAAGCTA TGC GACCGAA ACTTTGGGTA TTGGGTGCTG ATGGCGTCAT CTTCGTCCTG      300
CCGGGGGTCA ACGGCGCGGA CTACACTATG AGGATATTCA ACTCCGATGG CAGCAACCGG      360
AATGTNTGGN ATGGATTCGT TGCTTGCTCG CTTTATACGG AGTTGAAATC TACANGGAAA      420
CATACTTCAA AACAANAGGG GGCTGGATTA ATATCCTGAA ATANANACAT GNAAGTTANG      480
TNATATGGGC AACAATCTTA TGGCANATTT CANAAAATGC ATCACAAGAT AACTTNTAAA      540
ACGATTGAAT TAGGCAANAG AANTACCGTT ATAGGAACCC ATGAANCTTG TNAAATTAAG      600
GT                                                                    602
  
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: wlm24.pk0030.g4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Ala Leu His Phe Val Lys Tyr Gln Gly Leu Gly Asn Asp Phe Ile Met
1           5           10           15
Val Asp Asn Arg Asp Ser Ala Val Pro Lys Val Thr Pro Glu Glu Ala
20          25          30
Ala Lys Leu Cys Asp Arg Asn Phe Gly Xaa Gly Ala Asp Gly Val Ile
35          40          45
Phe Val Leu Pro Gly Val Asn Gly Ala Asp Tyr Thr Met Arg Ile Phe
50          55          60
  
```

Asn Ser Asp Gly Ser Asn Arg Asn Val Trp Xaa Gly Phe Val Ala Cys
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Synechocystus* sp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ala	Leu	Ser	Phe	Ser	Lys	Tyr	His	Gly	Leu	Gly	Asn	Asp	Phe	Ile	1	5	10	15
Leu	Val	Asp	Asn	Arg	Gln	Ser	Thr	Glu	Pro	Cys	Leu	Thr	Pro	Asp	Gln	20	25	30	
Ala	Gln	Gln	Leu	Cys	Asp	Arg	His	Phe	Gly	Ile	Gly	Ala	Asp	Gly	Val	35	40	45	
Ile	Phe	Ala	Leu	Pro	Gly	Gln	Gly	Gly	Thr	Asp	Tyr	Thr	Met	Arg	Ile	50	55	60	
Phe	Asn	Ser	Asp	Gly	Ser	Glu	Pro	Glu	Met	Cys	Gly	Asn	Gly	Ile	Arg	65	70	75	80
Cys	Leu	Ala	Lys	Phe	Leu	Ala	Asp	Leu	Glu	Gly	Val	Glu	Glu	Lys	Thr	85	90	95	
Tyr	Arg	Ile	His	Thr	Leu	Ala	Gly	Val	Ile	Thr	Pro	Gln	Leu	Leu	Ala	100	105	110	
Asp	Gly	Gln	Val	Lys	Val	Asp	Met	Gly	Glu	Pro	Gln	Leu	Leu	Ala	Glu	115	120	125	
Leu	Ile	Pro	Thr	Thr	Leu	Ala	Pro	Ala	Gly	Glu	Lys	Val	Val	Asp	Leu	130	135	140	
Pro	Leu	Ala	Val	Ala	Gly	Gln	Thr	Trp	Ala	Val	Thr	Cys	Val	Ser	Met	145	150	155	160
Gly	Asn	Pro	His	Cys	Leu	Thr	Phe	Val	Asp	Asp	Val	Asp	Ser	Leu	Asn	165	170	175	
Leu	Thr	Glu	Ile	Gly	Pro	Leu	Phe	Glu	His	His	Pro	Gln	Phe	Ser	Gln	180	185	190	
Arg	Thr	Asn	Thr	Glu	Phe	Ile	Gln	Val	Leu	Gly	Ser	Asp	Arg	Leu	Lys	195	200	205	
Met	Arg	Val	Trp	Glu	Arg	Gly	Ala	Gly	Ile	Thr	Leu	Ala	Cys	Gly	Thr	210	215	220	

Gly Ala Cys Ala Thr Val Val Ala Ala Val Leu Thr Gly Arg Gly Asp
 225 230 235 240

Arg Arg Cys Thr Val Glu Leu Pro Gly Gly Asn Leu Glu Ile Glu Trp
 245 250 255

Ser Ala Gln Asp Asn Arg Leu Tyr Met Thr Gly Pro Ala Gln Arg Val
 260 265 270

Phe Ser Gly Gln Ala Glu Ile
 275

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: cc2.pk0031.c9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTCGGCTGCG CGTCCACGGG AGACACCTCC GCCGCGCTCT CGGCCTACTG CGCAGCCGCG	60
GGAATCCCCG CCATCGTGTT CCTGCCAGCG GACCGCATCT CGCTGCAGCA GTCATCCAG	120
CCGATCGCCA ACGGCGCCAC CGTGCTCTCT CTAGACACTG ATTTTGATGG CTGCATGCGG	180
CTCATTCGCG AGGTCACTGC AGAGCTGCCA ATCTACCTTG CCAATTCGCT CAACCCGCTC	240
CGCCTTGAGG GGCAGAAGAC AGCGGCCATC GAGATATTGC AGCAGTTCAA TTGGCAGGTG	300
CCAGATTGGG TCATTGTTCC AGGAGGCAAT CTTGGGAATA TCTATGCATT CTACAAGGGG	360
TTTGAGATGT GCCGCGTTCT TGGACTTGTT GATCGCGTGC CACGGCTTGT CTGCGCACAG	420
GCTGCAAATG CAAATCCATT GTACCGGTAC TACAAGTCAG GTTGGACTGA GTTTGAGCCA	480
CAAAGTCCG AGACTACATT TGCATCTGCG ATACAGATTG GTGATCCTGT ATCTGTTGAC	540
CGTGCGGTGG TCGCGCTGAA GGCCACTGAC GGTATTGTGG AGGAGGCTAC AGAGGAGGAG	600
CTAATGGATG CAACGGCGCT TGCTGACCGC ACTGGGATGT TTGCTTGCCC ACATACTGGG	660
GTTGCACTTG CTGCTTTGTT TAAGCTTCAG GGTGAGCGTA TAATTGGCCC TAATGACCGC	720
ACTGTGTTTG TTAGCACAGC TCATGGGCTG AAGTTCACGC AGTCAAAGAT TGAATACCAT	780
GACAAAAACA TCAAAGACAT GGTTTGCCAG TATGCTAATC CACCGATCAG TGTGAAGGCT	840
GACTTTGGTT CTGTGATGGA TGTTCTCCAG AAAAATCTCA ATGGTAAGAT ATAAAGTTAT	900
ATGATTAATT AACCTCCAA ACTGTTTTTT TTTGTTTTTT CGTTCCAGGA ATTTTATTCC	960

TGAGTCTTTC AACTTTGTTT GGTGAACATG GTATGGTGCT AAAATCTAGA CCTAATACCT 1020
 TGTAGTACTA GTTCTGGAGG CTCTTTTGGT TGTAGGTCGA AGTGGATAGA GCTGTTTCCTT 1080
 GTACTTTATC TGTTTCATGT AATATGAATA ATAAATTATG GTCTAAATAT TTGAATAAAA 1140
 AATCGTTTGG AATGACCCAC 1160

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: cc2.pk0031.c9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val	Gly	Cys	Ala	Ser	Thr	Gly	Asp	Thr	Ser	Ala	Ala	Leu	Ser	Ala	Tyr	1	5	10	15
Cys	Ala	Ala	Ala	Gly	Ile	Pro	Ala	Ile	Val	Phe	Leu	Pro	Ala	Asp	Arg	20	25	30	
Ile	Ser	Leu	Gln	Gln	Leu	Ile	Gln	Pro	Ile	Ala	Asn	Gly	Ala	Thr	Val	35	40	45	
Leu	Ser	Leu	Asp	Thr	Asp	Phe	Asp	Gly	Cys	Met	Arg	Leu	Ile	Arg	Glu	50	55	60	
Val	Thr	Ala	Glu	Leu	Pro	Ile	Tyr	Leu	Ala	Asn	Ser	Leu	Asn	Pro	Leu	65	70	75	80
Arg	Leu	Glu	Gly	Gln	Lys	Thr	Ala	Ala	Ile	Glu	Ile	Leu	Gln	Gln	Phe	85	90	95	
Asn	Trp	Gln	Val	Pro	Asp	Trp	Val	Ile	Val	Pro	Gly	Gly	Asn	Leu	Gly	100	105	110	
Asn	Ile	Tyr	Ala	Phe	Tyr	Lys	Gly	Phe	Glu	Met	Cys	Arg	Val	Leu	Gly	115	120	125	
Leu	Val	Asp	Arg	Val	Pro	Arg	Leu	Val	Cys	Ala	Gln	Ala	Ala	Asn	Ala	130	135	140	
Asn	Pro	Leu	Tyr	Arg	Tyr	Tyr	Lys	Ser	Gly	Trp	Thr	Glu	Phe	Glu	Pro	145	150	155	160
Gln	Thr	Ala	Glu	Thr	Thr	Phe	Ala	Ser	Ala	Ile	Gln	Ile	Gly	Asp	Pro	165	170	175	
Val	Ser	Val	Asp	Arg	Ala	Val	Val	Ala	Leu	Lys	Ala	Thr	Asp	Gly	Ile	180	185	190	

Val	Glu	Glu	Ala	Thr	Glu	Glu	Glu	Leu	Met	Asp	Ala	Thr	Ala	Leu	Ala	
			195					200					205			
Asp	Arg	Thr	Gly	Met	Phe	Ala	Cys	Pro	His	Thr	Gly	Val	Ala	Leu	Ala	
			210				215					220				
Ala	Leu	Phe	Lys	Leu	Gln	Gly	Gln	Arg	Ile	Ile	Gly	Pro	Asn	Asp	Arg	
			225				230				235				240	
Thr	Val	Val	Val	Ser	Thr	Ala	His	Gly	Leu	Lys	Phe	Thr	Gln	Ser	Lys	
				245					250					255		
Ile	Asp	Tyr	His	Asp	Lys	Asn	Ile	Lys	Asp	Met	Val	Cys	Gln	Tyr	Ala	
			260					265					270			
Asn	Pro	Pro	Ile	Ser	Val	Lys	Ala	Asp	Phe	Gly	Ser	Val	Met	Asp	Val	
			275				280					285				
Leu	Gln	Lys	Asn	Leu	Asn	Gly	Lys	Ile								
			290				295									

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: cs1.pk0058.g5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGGCTTGCA AGTACTCCAA CCCGCCTGTG AGCGTGAAGG CTGACTTTGG CGCCGTGATG	60
GATGTGCTGA AGAAGAGGCT CAAGGGCAAG CTCTGAGCGC CTGTGCCTGG CTAATGCAAT	120
CAACTGATTG GAATGCAGTG GTTTCGTCGG TATCGGGGGG TCTTTTAGGC TTCAGAAATT	180
CTGTCTGGGT TAGACTATTT GTTTGTGGAG TTTAGCAGGA GAATGGCTAT CTCTCCTGCA	240
AGACTGGCGC TCTTCTTGT GCTACGAATG TGTTACCATG GATAATAAGT GTAGTCGCTG	300
TCGGATTGAA TAATCAAAAA AAAAN	325

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: cs1.pk0058.g5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Cys Lys Tyr Ser Asn Pro Pro Val Ser Val Lys Ala Asp Phe
1 5 10 15

Gly Ala Val Met Asp Val Leu Lys Lys Arg Leu Lys Gly Lys Leu
20 25 30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 528 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: rls72.pk0018.e7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACACCCAACA CGCAGACTTG ACAGATTCTG CTACTACAAA TCCTGCATAT TTAACAGCGC 60
TGCAACTCGA CGATGGAGAA CGGTGCTGCA ACCAACGGGG CGTCGGAGAA GTCGCACTCT 120
CCTTCACAGA CCTACCTCTC CACAAGGGGA GACGATTATG GGCTCTCATT CGAGACCGTC 180
GTCCTCAAAG GTCTTGCGGC TGACGGGGGT CTTTTCCTGC CCGAGGAAGT GCCCCGCGCA 240
ACCGAGTGGC AAAGCTGGAA AGACCTGCCC TACACCGAGC TTGCCGTCAA GGTTCCTCAGC 300
TTGTACATCT CCCCCGCCGA GGTGCCGACG GAAGACCTCA GGGCGCTCGT CGAGCGCAGC 360
TACTCGACCT TCCGATCCAA GGAGGTTGTG CCGCTGGTGA AGCTGGAGGA CAACCTTCAC 420
CTGCTGGAGC TATTCCACGG CCCCAACTAC TCGTTCAAGG ACTGCGCGCT GCAATTCCTT 480
GGTAACCTCN TCGAGTACTT TTGACTCNCA AGAACAAGGG AAAGGAGG 528

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: rls72.pk0018.e7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Glu Asn Gly Ala Ala Thr Asn Gly Ala Ser Glu Lys Ser His Ser
1 5 10 15

Pro Ser Gln Thr Tyr Leu Ser Thr Arg Gly Asp Asp Tyr Gly Leu Ser
 20 25 30
 Phe Glu Thr Val Val Leu Lys Gly Leu Ala Ala Asp Gly Gly Leu Phe
 35 40 45
 Leu Pro Glu Glu Val Pro Ala Ala Thr Glu Trp Gln Ser Trp Lys Asp
 50 55 60
 Leu Pro Tyr Thr Glu Leu Ala Val Lys Val Leu Ser Leu Tyr Ile Ser
 65 70 75 80
 Pro Ala Glu Val Pro Thr Glu Asp Leu Arg Ala Leu Val Glu Arg Ser
 85 90 95
 Tyr Ser Thr Phe Arg Ser Lys Glu Val Val Pro Leu Val Lys Leu Glu
 100 105 110
 Asp Asn Leu His Leu Leu Glu Leu Phe His Gly Pro Asn Tyr Ser Phe
 115 120 125
 Lys Asp Cys Ala Leu Gln Phe Leu Gly Asn Leu Xaa Glu Tyr Phe
 130 135 140

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: se1.06a03

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGATGCAATG GTGCAGGCTG ATTCCACTGG AATGTTTCATA TGTCCACACA CTGGGGTGGC	60
TCTGGCGGCG CTTATTAAGC TGAGGAATCG TGGGGTTATC GGTGCCGGTG AGAGGGTTGT	120
GGTGGTGAGC ACTGCACATG GATTGAAGTT TGCACAGAGC AAGATTGATT ATCATTTCTGG	180
GCTCATTCCT GGAATGGGCC GCTATGCTAA CCCGCTGGTT TCGGTTAAGG CGGATTTTGG	240
ATCGGTCATG GATGTTCTCA AGGATTCTTG CACAACAAGT CCCCCGACTT TAACAAGTCT	300
TGACGTTGCC AAGTAAGTTT TAGTTCGGGG TTTTTTCTGA TTAAAGATGT TTTTAAACAT	360
GTTTGTGTNC ACTTTCGGTC GTTATTATGG ATTTGTAAGA TTGGGCCCAA GTATTTCGAGG	420
GTTTGATTTT AAACAACATG CTTCTGGTGA CGCAATGCAA ATTTTCGGNGC ATAACATCAT	480
TGTCGAAGAT GGATCNCGAC CGATGAAACT GTGTGGCAAG TAATGAGAAG AAAATAGGGC	540
ACTTGTACAG AGATTTNAAA GNTTAATTTT N	571

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: se1.06a03

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Asp Ala Met Val Gln Ala Asp Ser Thr Gly Met Phe Ile Cys Pro His
1           5           10           15
Thr Gly Val Ala Leu Ala Ala Leu Ile Lys Leu Arg Asn Arg Gly Val
20          25          30
Ile Gly Ala Gly Glu Arg Val Val Val Val Ser Thr Ala His Gly Leu
35          40          45
Lys Phe Ala Gln Ser Lys Ile Asp Tyr His Ser Gly Leu Ile Pro Gly
50          55          60
Met Gly Arg Tyr Ala Asn Pro Leu Val Ser Val Lys Ala Asp Phe Gly
65          70          75          80
Ser Val Met Asp Val Leu Lys Asp Ser Cys Thr Thr Ser Pro Pro Thr
85          90          95
Leu Thr Ser Leu Asp Val Ala Lys
100

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2191 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: sr1.pk0003.f6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

GCTTCCTCTT CTCTGTTTCA GTCTCTCCCT TTCTCTCTCC AACCTCTAA ACCCTACGCG      60
CCTCCCAAAC CCGCCGCCCA CTTCGTTGTC CGCGCCCAAT CCCCCTCAC TCAGAACAAAC      120
AACTCCTCCT CCAAGCATCG CCGCCCCGCC GACGAGAACA TCCGCGACGA GGCCCGCCGC      180
ATCAATGCGC CCCACGACCA CCACCTCTTC TCGGCCAAGT ACGTCCCCTT CAACGCCGAC      240
TCCTCCTCCT CCTCCTCCAC GGAGTCCTAC TCGCTCGACG AGATCGTCTA CCGCTCCCAA      300

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TCCGGCGGCC	TCCTGGACGT	CCAGCACGAC	ATGGATGCCC	TCAAGCGTTT	CGACGGCGAG	360
TACTGGCGCA	ACCTCTTCGA	CTCGCGCGTG	GGCAAAACCA	CCTGGCCTTA	CGGCTCCGGC	420
GTCTGGAGCA	AAAAAGAATG	GGTCCTCCCC	GAGATCCACG	ACGACGATAT	CGTCTCCGCC	480
TTCGAGGGTA	ACTCCAACCT	CTTCTGGGCC	GAGCGTTTCG	GCAAACAGTT	CCTCGGCATG	540
AACGATTTGT	GGGTCAAACA	CTGCGGAATC	AGCCACACGG	GCAGCTTCAA	GGATCTCGGC	600
ATGACCGTCC	TCGTACAGCA	GGTCAATCGC	TTGAGAAAAA	TGAACCGCCC	CGTCGTCGGT	660
GTTGGTTGCG	CCTCCACCGG	TGACACATCG	GCCGCTTTAT	CCGCCTATTG	CGCTTCCGCT	720
GCCATTCCCT	CCATTGTGTT	TTTGCTGCT	AATAAAATCT	CTCTTGCCCA	ACTTGTTTCA	780
CCTATTGCCA	ATGGAGCCTT	TGTGTTGAGT	ATCGACACTG	ATTTTGATGG	TTGCATGCAG	840
TTGATCAGAG	AAGTCACTGC	TGAATTGCCT	ATTTATTTGG	CTAACTCTCT	CAACAGTTTG	900
AAGTTGGAAG	GGCAGAAAAC	TGCTGCTATT	GAGATTCTGC	AGCAGTTTGA	TTGGCAGGTT	960
CCTGATTGGG	TCATTGTGCC	TGGAAGCAAC	CTTGGAACA	TTTATGCCTT	TTACAAAGGG	1020
TTTAAGATGT	TTCAAGAGCT	TGGGCTTGTG	GATAAGATTC	CAAGGCTTGT	TTGTGCTCAG	1080
GCTGCCAATG	CTGATCCTTT	GTATTTGTAC	TTTAAATCCG	GGTGGAAGGA	GTTTAAGCCT	1140
GTGAAGTCGA	GCACTACATT	TGCTTCTGCC	ATTCAAATTG	GTGATCCTGT	TTCCATTGAC	1200
AGGGCGGTTT	ACGCGCTAAA	GAGTTGCGAT	GGGATTGTGG	AGGAGGCCAC	GGAGGAGGAG	1260
TTGATGGATG	CTACAGCGCA	GGCGGATTCT	ACTGGGATGT	TTATTTGCCC	CCACACCGGG	1320
GTTGCTTTAA	CTGCATTGTT	TAAGCTCAGG	AACAGCGGGG	TTATTAAGGC	CACTGATAGG	1380
ACTGTGGTGG	TTAGCACTGC	TCATGGCTTG	AAGTTCCTC	AGTCCAAGAT	TGATTACCAT	1440
TCTAAGGACA	TCAAGGACAT	GGCTTGCCGC	TATGCTAACC	CGCCCATGCA	AGTGAAGGCA	1500
GACTTTGGCT	CGGTTATGGA	TGTTTTGAAG	ACGTATTTGC	AGAGTAAGGC	TCATTAGGTT	1560
AGCATTGCAA	GTTTTGCTCC	TCCTGAGTTT	GCTCATTATT	TACTTACTTT	TAGGCACTAC	1620
TGCTGTATTG	TCTTTTCTAT	GAGCTAGGTT	TGAGTGTGTT	AATAATTTGC	TTGCTGCATT	1680
ATGTATGCCG	TCTAGTGTTT	CATATTGGGC	ATCATCCTTA	GTATTTGTTG	TAGATTTTCT	1740
TTGCTGAGCA	TTTGATATAA	TAGCTCAAGT	AGGAAAATGA	ATTGGGTACT	ATGAGGAATG	1800
CATATCATTG	GCTTGTTATT	ACTGGATTCC	AGACCACCCC	AAAAGAAAAT	AATTCCAAAA	1860
AATATAATTA	GAACAAATTT	CGTCCTTGTT	ATGCTGTTGG	CATTAAGCTC	AGTGTGGGTA	1920
TTACCAAGCA	ACTCGAAATC	AAGAGAAAAA	AAAATTGACA	GCAAAGGAGC	TGCATTGTTG	1980
GA CTGAGTCA	CATCACTTCA	TTGCTATGTC	GTCATATTTT	GTTGAATTAC	GGGAAGGCAG	2040
CATGCACAGC	AATATGCAGC	GATTAAGTGA	AGCCACACCG	CACACATTGA	AGTAGTAGTC	2100

AATTTAGACA CTCCATCTTG TACTTTCTAC AAAAATGAAT TTTTCTTAGC CATTAAGTAT 2160
 AATATTTTAT TCTAAAAAAA AAAAAAAAAA A 2191

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 518 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: sr1.pk0003.f6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ala	Ser	Ser	Ser	Leu	Phe	Gln	Ser	Leu	Pro	Phe	Ser	Leu	Gln	Thr	Ser	1	5	10	15
Lys	Pro	Tyr	Ala	Pro	Pro	Lys	Pro	Ala	Ala	His	Phe	Val	Val	Arg	Ala	20	25	30	
Gln	Ser	Pro	Leu	Thr	Gln	Asn	Asn	Asn	Ser	Ser	Ser	Lys	His	Arg	Arg	35	40	45	
Pro	Ala	Asp	Glu	Asn	Ile	Arg	Asp	Glu	Ala	Arg	Arg	Ile	Asn	Ala	Pro	50	55	60	
His	Asp	His	His	Leu	Phe	Ser	Ala	Lys	Tyr	Val	Pro	Phe	Asn	Ala	Asp	65	70	75	80
Ser	Ser	Ser	Ser	Ser	Ser	Thr	Glu	Ser	Tyr	Ser	Leu	Asp	Glu	Ile	Val	85	90	95	
Tyr	Arg	Ser	Gln	Ser	Gly	Gly	Leu	Leu	Asp	Val	Gln	His	Asp	Met	Asp	100	105	110	
Ala	Leu	Lys	Arg	Phe	Asp	Gly	Glu	Tyr	Trp	Arg	Asn	Leu	Phe	Asp	Ser	115	120	125	
Arg	Val	Gly	Lys	Thr	Thr	Trp	Pro	Tyr	Gly	Ser	Gly	Val	Trp	Ser	Lys	130	135	140	
Lys	Glu	Trp	Val	Leu	Pro	Glu	Ile	His	Asp	Asp	Asp	Ile	Val	Ser	Ala	145	150	155	160
Phe	Glu	Gly	Asn	Ser	Asn	Leu	Phe	Trp	Ala	Glu	Arg	Phe	Gly	Lys	Gln	165	170	175	
Phe	Leu	Gly	Met	Asn	Asp	Leu	Trp	Val	Lys	His	Cys	Gly	Ile	Ser	His	180	185	190	
Thr	Gly	Ser	Phe	Lys	Asp	Leu	Gly	Met	Thr	Val	Leu	Val	Ser	Gln	Val	195	200	205	
Asn	Arg	Leu	Arg	Lys	Met	Asn	Arg	Pro	Val	Val	Gly	Val	Gly	Cys	Ala	210	215	220	

Ser	Thr	Gly	Asp	Thr	Ser	Ala	Ala	Leu	Ser	Ala	Tyr	Cys	Ala	Ser	Ala	225	230	235	240
Ala	Ile	Pro	Ser	Ile	Val	Phe	Leu	Pro	Ala	Asn	Lys	Ile	Ser	Leu	Ala	245	250	255	
Gln	Leu	Val	Gln	Pro	Ile	Ala	Asn	Gly	Ala	Phe	Val	Leu	Ser	Ile	Asp	260	265	270	
Thr	Asp	Phe	Asp	Gly	Cys	Met	Gln	Leu	Ile	Arg	Glu	Val	Thr	Ala	Glu	275	280	285	
Leu	Pro	Ile	Tyr	Leu	Ala	Asn	Ser	Leu	Asn	Ser	Leu	Lys	Leu	Glu	Gly	290	295	300	
Gln	Lys	Thr	Ala	Ala	Ile	Glu	Ile	Leu	Gln	Gln	Phe	Asp	Trp	Gln	Val	305	310	315	320
Pro	Asp	Trp	Val	Ile	Val	Pro	Gly	Ser	Asn	Leu	Gly	Asn	Ile	Tyr	Ala	325	330	335	
Phe	Tyr	Lys	Gly	Phe	Lys	Met	Phe	Gln	Glu	Leu	Gly	Leu	Val	Asp	Lys	340	345	350	
Ile	Pro	Arg	Leu	Val	Cys	Ala	Gln	Ala	Ala	Asn	Ala	Asp	Pro	Leu	Tyr	355	360	365	
Leu	Tyr	Phe	Lys	Ser	Gly	Trp	Lys	Glu	Phe	Lys	Pro	Val	Lys	Ser	Ser	370	375	380	
Thr	Thr	Phe	Ala	Ser	Ala	Ile	Gln	Ile	Gly	Asp	Pro	Val	Ser	Ile	Asp	385	390	395	400
Arg	Ala	Val	His	Ala	Leu	Lys	Ser	Cys	Asp	Gly	Ile	Val	Glu	Glu	Ala	405	410	415	
Thr	Glu	Glu	Glu	Leu	Met	Asp	Ala	Thr	Ala	Gln	Ala	Asp	Ser	Thr	Gly	420	425	430	
Met	Phe	Ile	Cys	Pro	His	Thr	Gly	Val	Ala	Leu	Thr	Ala	Leu	Phe	Lys	435	440	445	
Leu	Arg	Asn	Ser	Gly	Val	Ile	Lys	Ala	Thr	Asp	Arg	Thr	Val	Val	Val	450	455	460	
Ser	Thr	Ala	His	Gly	Leu	Lys	Phe	Thr	Gln	Ser	Lys	Ile	Asp	Tyr	His	465	470	475	480
Ser	Lys	Asp	Ile	Lys	Asp	Met	Ala	Cys	Arg	Tyr	Ala	Asn	Pro	Pro	Met	485	490	495	
Gln	Val	Lys	Ala	Asp	Phe	Gly	Ser	Val	Met	Asp	Val	Leu	Lys	Thr	Tyr	500	505	510	
Leu	Gln	Ser	Lys	Ala	His											515			

(2) INFORMATION FOR SEQ ID NO:25:

Lys Thr Ala Ala Ile Arg Asp Ile Ala Thr Xaa Asn Trp Gln Val Pro
 50 55 60

Gly Leu Gly His Ile Pro Arg Arg Gln Ser Xaa Thr Phe Tyr Ala Phe
 65 70 75 80

Leu Gln Gly Phe

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 525 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu Ser Ser Cys Leu Phe Asn Ala Ser Val Ser Ser Leu Asn Pro Lys
 1 5 10 15

Gln Asp Pro Ile Arg Arg His Arg Ser Thr Ser Leu Leu Arg His Arg
 20 25 30

Pro Val Val Ile Ser Cys Thr Ala Asp Gly Asn Asn Ile Lys Ala Pro
 35 40 45

Ile Glu Thr Ala Val Lys Pro Pro His Arg Thr Glu Asp Asn Ile Arg
 50 55 60

Asp Glu Ala Arg Arg Asn Arg Ser Asn Ala Val Asn Pro Phe Ser Ala
 65 70 75 80

Lys Tyr Val Pro Phe Asn Ala Ala Pro Gly Ser Thr Glu Ser Tyr Ser
 85 90 95

Leu Asp Glu Ile Val Tyr Arg Ser Arg Ser Gly Gly Leu Leu Asp Val
 100 105 110

Glu His Asp Met Glu Ala Leu Lys Arg Phe Asp Gly Ala Tyr Trp Arg
 115 120 125

Asp Leu Phe Asp Ser Arg Val Gly Lys Ser Thr Trp Pro Tyr Gly Ser
 130 135 140

Gly Val Trp Ser Lys Lys Glu Trp Val Leu Pro Glu Ile Asp Asp Asp
 145 150 155 160

Asp Ile Val Ser Ala Phe Glu Gly Asn Ser Asn Leu Phe Trp Ala Glu
 165 170 175

Arg Phe Gly Lys Gln Phe Leu Gly Met Asn Asp Leu Trp Val Lys His
 180 185 190

Cys	Gly	Ile	Ser	His	Thr	Gly	Ser	Phe	Lys	Asp	Leu	Gly	Met	Thr	Val	195	200	205
Leu	Val	Ser	Gln	Val	Asn	Arg	Leu	Arg	Lys	Met	Lys	Arg	Pro	Val	Val	210	215	220
Gly	Val	Gly	Cys	Ala	Ser	Thr	Gly	Asp	Thr	Ser	Ala	Ala	Leu	Ser	Ala	225	230	235
Tyr	Cys	Ala	Ser	Ala	Gly	Ile	Pro	Ser	Ile	Val	Phe	Leu	Pro	Ala	Asn	245	250	255
Lys	Ile	Ser	Met	Ala	Gln	Leu	Val	Gln	Pro	Ile	Ala	Asn	Gly	Ala	Phe	260	265	270
Val	Leu	Ser	Ile	Asp	Thr	Asp	Phe	Asp	Gly	Cys	Met	Lys	Leu	Ile	Arg	275	280	285
Glu	Ile	Thr	Ala	Glu	Leu	Pro	Ile	Tyr	Leu	Ala	Asn	Ser	Leu	Asn	Ser	290	295	300
Leu	Arg	Leu	Glu	Gly	Gln	Lys	Thr	Ala	Ala	Ile	Glu	Ile	Leu	Gln	Gln	305	310	315
Phe	Asp	Trp	Gln	Val	Pro	Asp	Trp	Val	Ile	Val	Pro	Gly	Gly	Asn	Leu	325	330	335
Gly	Asn	Ile	Tyr	Ala	Phe	Tyr	Lys	Gly	Phe	Lys	Met	Cys	Gln	Glu	Leu	340	345	350
Gly	Leu	Val	Asp	Arg	Ile	Pro	Arg	Met	Val	Cys	Ala	Gln	Ala	Ala	Asn	355	360	365
Ala	Asn	Pro	Leu	Tyr	Leu	His	Tyr	Lys	Ser	Gly	Trp	Lys	Asp	Phe	Lys	370	375	380
Pro	Met	Thr	Ala	Ser	Thr	Thr	Phe	Ala	Ser	Ala	Ile	Gln	Ile	Gly	Asp	385	390	395
Pro	Val	Ser	Ile	Asp	Arg	Ala	Val	Tyr	Ala	Leu	Lys	Lys	Cys	Asn	Gly	405	410	415
Ile	Val	Glu	Glu	Ala	Thr	Glu	Glu	Glu	Leu	Met	Asp	Ala	Met	Ala	Gln	420	425	430
Ala	Asp	Ser	Thr	Gly	Met	Phe	Ile	Cys	Pro	His	Thr	Gly	Val	Ala	Leu	435	440	445
Thr	Ala	Leu	Phe	Lys	Leu	Arg	Asn	Gln	Gly	Val	Ile	Ala	Pro	Thr	Asp	450	455	460
Arg	Thr	Val	Val	Val	Ser	Thr	Ala	His	Gly	Leu	Lys	Phe	Thr	Gln	Ser	465	470	475
Lys	Ile	Asp	Tyr	His	Ser	Asn	Ala	Ile	Pro	Asp	Met	Ala	Cys	Arg	Phe	485	490	495
Ser	Asn	Pro	Pro	Val	Asp	Val	Lys	Ala	Asp	Phe	Gly	Ala	Val	Met	Asp	500	505	510

Val Leu Lys Ser Tyr Leu Gly Ser Asn Thr Leu Thr Ser
515 520 525

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: cen1.pk0064.f4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAACAGTGGT CCTTGAGGGG GACTCATATG ATGAAGCTCA GTCATATGCA AAATTGCGTT	60
GCCAGCAGGA AGGCCGCACA TTTGTACCTC CTTTTGACCA TCCTGATGTC ATCACTGGAC	120
AAGGAACTAT CGGCATGGAA ATTGTTAGGC AGCTGCAAGG TCCACTGCAT GCAATATTTG	180
TACCTGTTGG AGGTGGTGGG TTAATTGCTG GAATTGCTGC CTATGTAAAA CGGGTTCGCC	240
CAGAGGTGAA AATAATTGGA GTGGAACCCT CAGATGCAAA TGCAATGGCA TTATCCTTGT	300
GTCATGGTAA GAGGGTCATG TTGGAGCATG TTGGTGGGTT TGCTGATGGT GTAGCTGTCA	360
AAGCTGTTGG GGAAGAAACA TTTTCGCCTGT GCAGAGAGCT AGTAGATGGC ATTGTTATGG	420
TCAGTCGAGA TGCTATTTGT GCTTCAATAA AGGATATGTT TGAGGAGAAA AGAAGTATCC	480
TTGAACCTGC TGGTGCCCTT GCATTGGCTG GGGCTGAAGC CTA CTGCAAA TACTATAACT	540
TGAAAGGAGA AACTGTGGTT GCAATAACTA GTGGGGGCAAA TATGAACTTT GATCGACTTA	600
GACTAGTAAC CGAGCTAGCT GATGTTGGCC GAAAACGGGA AGCAGTGTTA GCTACATTTT	660
TGCCAGAGCG GCAGGGAAGC TTCAAAAAAT TCACAGAATT GGTGGCAGG ATGAATATTA	720
CTGAATTCAA ATACAGATAC GATTCTAATG CAAAAGATGC CCTTGTTCTT TACAGTGTG	780
GCATCTACAC TGACAATGAG CTTGGAGCAA TGATGGATCG CATGGAATCT GCGAAACTGA	840
GGACTGTTAA CCTTACTGAC AATGATTTGG CAAAGGACCA CCTTAGATAC TTTATTGGAG	900
GAAGATCAGA AATAAAAGAT GAACTGGTTT ACCGGTTCAT TTTCCCGGAA AGGCCTGGGG	960
CCCTTATGAA ATTTTTGGAC ACGTTTAGTC CTCGTTGGAA CATCAGCCTT TTCCATTACC	1020
GTGCACAGGG TGAAGCTGGA GCAAATGTAT TAGTTGGTAT ACAAGTGCCG CCAGCAGAAT	1080
TTGATGAATT CAAGAGTCAT GCCAACAATC TTGGGTACGA GTACATGTCA GAGCACAACA	1140
ATGAGATATA CCGGTTGCTG TTGCGTGACC CAAAGGTCTA ATGTATATGC CTTTGCTCCC	1200
ATAATAAGTT GGTGACACTT TTCAAGGAAG ATTTTGCTCC AAGGTAGAAG TTGCGAGTTT	1260

CTTCAAGTTG AAATGAAGCC ATCACCAAAT GTAGCTTCGG TGTGCCATCT GTTTACTCAG 1320
 TTAGATCATG TAGTGTATCA GTTGTGTATC TTTGTTGTTG TGCTTCGTGA TCTCAATTTA 1380
 TTGCTTTGTG CACCTAGAGG TTGTCAAATA ATGATAACCG ATATGTTATC TAAATATCTA 1440
 ATAATGATTA TGTGATTGTG ATTAAAAAGG GGGGGCCC 1478

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 392 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: cen1.pk0064.f4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Thr	Val	Val	Leu	Glu	Gly	Asp	Ser	Tyr	Asp	Glu	Ala	Gln	Ser	Tyr	Ala	1	5	10	15
Lys	Leu	Arg	Cys	Gln	Gln	Glu	Gly	Arg	Thr	Phe	Val	Pro	Pro	Phe	Asp	20	25	30	
His	Pro	Asp	Val	Ile	Thr	Gly	Gln	Gly	Thr	Ile	Gly	Met	Glu	Ile	Val	35	40	45	
Arg	Gln	Leu	Gln	Gly	Pro	Leu	His	Ala	Ile	Phe	Val	Pro	Val	Gly	Gly	50	55	60	
Gly	Gly	Leu	Ile	Ala	Gly	Ile	Ala	Ala	Tyr	Val	Lys	Arg	Val	Arg	Pro	65	70	75	80
Glu	Val	Lys	Ile	Ile	Gly	Val	Glu	Pro	Ser	Asp	Ala	Asn	Ala	Met	Ala	85	90	95	
Leu	Ser	Leu	Cys	His	Gly	Lys	Arg	Val	Met	Leu	Glu	His	Val	Gly	Gly	100	105	110	
Phe	Ala	Asp	Gly	Val	Ala	Val	Lys	Ala	Val	Gly	Glu	Glu	Thr	Phe	Arg	115	120	125	
Leu	Cys	Arg	Glu	Leu	Val	Asp	Gly	Ile	Val	Met	Val	Ser	Arg	Asp	Ala	130	135	140	
Ile	Cys	Ala	Ser	Ile	Lys	Asp	Met	Phe	Glu	Glu	Lys	Arg	Ser	Ile	Leu	145	150	155	160
Glu	Pro	Ala	Gly	Ala	Leu	Ala	Leu	Ala	Gly	Ala	Glu	Ala	Tyr	Cys	Lys	165	170	175	
Tyr	Tyr	Asn	Leu	Lys	Gly	Glu	Thr	Val	Val	Ala	Ile	Thr	Ser	Gly	Ala	180	185	190	

Asn	Met	Asn	Phe	Asp	Arg	Leu	Arg	Leu	Val	Thr	Glu	Leu	Ala	Asp	Val	
		195					200					205				
Gly	Arg	Lys	Arg	Glu	Ala	Val	Leu	Ala	Thr	Phe	Leu	Pro	Glu	Arg	Gln	
	210					215					220					
Gly	Ser	Phe	Lys	Lys	Phe	Thr	Glu	Leu	Val	Gly	Arg	Met	Asn	Ile	Thr	
225					230					235					240	
Glu	Phe	Lys	Tyr	Arg	Tyr	Asp	Ser	Asn	Ala	Lys	Asp	Ala	Leu	Val	Leu	
				245					250					255		
Tyr	Ser	Val	Gly	Ile	Tyr	Thr	Asp	Asn	Glu	Leu	Gly	Ala	Met	Met	Asp	
			260					265					270			
Arg	Met	Glu	Ser	Ala	Lys	Leu	Arg	Thr	Val	Asn	Leu	Thr	Asp	Asn	Asp	
		275					280					285				
Leu	Ala	Lys	Asp	His	Leu	Arg	Tyr	Phe	Ile	Gly	Gly	Arg	Ser	Glu	Ile	
	290					295					300					
Lys	Asp	Glu	Leu	Val	Tyr	Arg	Phe	Ile	Phe	Pro	Glu	Arg	Pro	Gly	Ala	
305					310					315					320	
Leu	Met	Lys	Phe	Leu	Asp	Thr	Phe	Ser	Pro	Arg	Trp	Asn	Ile	Ser	Leu	
				325					330					335		
Phe	His	Tyr	Arg	Ala	Gln	Gly	Glu	Ala	Gly	Ala	Asn	Val	Leu	Val	Gly	
			340					345					350			
Ile	Gln	Val	Pro	Pro	Ala	Glu	Phe	Asp	Glu	Phe	Lys	Ser	His	Ala	Asn	
		355					360					365				
Asn	Leu	Gly	Tyr	Glu	Tyr	Met	Ser	Glu	His	Asn	Asn	Glu	Ile	Tyr	Arg	
	370					375					380					
Leu	Leu	Leu	Arg	Asp	Pro	Lys	Val									
385						390										

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: sfl1.pk0055.h7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAATATTGT AGCAATAACC AGTGGAGCAA ACATGAATTT TGATAAACTT CGGGTTGTAA	60
CTGAACTTGC TAATGTTGGT CGTAAACAAG AGGCTGTGCT GGCAACTGTT ATGGCAGAGG	120
AGCCTGGCAG TTTCAAACAA TTTTGTGAAT TGGTGGGGCA GATGAACATA ACAGAATTCA	180

AATACAGATA	TAACTCAAAT	GAGAAGGCAG	TTGTCCTTTA	CAGTGTTGGG	GTTCACACAA	240
TCTCCGAAC	AAGAGCAATG	CAGGAGAGGA	TGGAATCTTC	TCAGCTCAAA	ACTTACAATC	300
TCACAGAAAG	TGACTTGGTG	AAAGACCACT	TGCGTTACTT	GATGGGAGGC	CGATCAAACG	360
TTCAGAATGA	GGTCTTTGTC	GTCTCACCTT	TCCAAGAAAG	ACTGGTGCTT	TGATGAAATT	420
TTTGGACCCT	TCAGTCCACG	TTGGGATATT	AGTTTATCCA	TTACCGAGGG	GAGGTGAAAC	480
TGGAGCAAAC	TGCTAGTTGG	NTACAGGTAC	CAAATGAGA	TAGATGAGTC	CATGATCGTG	540
CTAACAAACT	GGATATGATT	ATAAGTGGNA	ATATGTGATG	NCTCAGCTCA	ATCNCGATGG	600
GGNTTAAGCA	CTGCATATGG	GNATTAGGGG	NAGNTACANT	TAAATTCACG	GCCTCAAGNT	660
AAGCATANTN	TAGGAACTAG	CTTTACAGGG	GGCTACNANT	TAACCGNGTA	TTTTTTTTGA	720
GATGANNG						728

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: sfl1.pk0055.h7

Asn	Ile	Val	Ala	Ile	Thr	Ser	Gly	Ala	Asn	Met	Asn	Phe	Asp	Lys	Leu
1				5					10					15	
Arg	Val	Val	Thr	Glu	Leu	Ala	Asn	Val	Gly	Arg	Lys	Gln	Glu	Ala	Val
			20					25					30		
Leu	Ala	Thr	Val	Met	Ala	Glu	Glu	Pro	Gly	Ser	Phe	Lys	Gln	Phe	Cys
		35					40					45			
Glu	Leu	Val	Gly	Gln	Met	Asn	Ile	Thr	Glu	Phe	Lys	Tyr	Arg	Tyr	Asn
	50					55					60				
Ser	Asn	Glu	Lys	Ala	Val	Val	Leu	Tyr	Ser	Val	Gly	Val	His	Thr	Ile
65					70					75					80
Ser	Glu	Leu	Arg	Ala	Met	Gln	Glu	Arg	Met	Glu	Ser	Ser	Gln	Leu	Lys
				85					90					95	
Thr	Tyr	Asn	Leu	Thr	Glu	Ser	Asp	Leu	Val	Lys	Asp	His	Leu	Arg	Tyr
			100					105					110		
Leu	Met	Gly	Gly	Arg	Ser	Asn	Val	Gln	Asn	Glu	Val	Phe	Val	Val	Ser
		115					120					125			

Pro Xaa Pro Arg Lys Thr Gly Ala Leu Met Lys Phe Leu Asp Xaa Phe
 130 135 140

Ser Pro Arg Trp Asp Ile Ser Leu
 145 150

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: sre.pk0044.f3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AAAGACCTGG TGCTTTGATG AAATTTTGG ACCCCTTCAG TCCACGTTGG AATATCAGTT	60
TATTCATTA CCGAGGGGAG GGTGAAACTG GAGCAAATGT GCTAGTTGGA ATACAGGTAC	120
CCAAAAGTGA GATGGATGAG TTCCACGATC GTGCCAACAA ACTTGGATAT GATTATAAAG	180
TGGTGAATAA TGATGATGAC TTCCAGCTTC TAATGCACTG ATGATGGTTT TAGGCACTTG	240
CCATTATTGT GTATTTTAGT CAACAAGTTT GCCATATTTA ATATTTCCAC GGTTCGTTTCT	300
AAAAGTTGGA TGGGGAAAAA AGGTGGAAAG GAAGTGGCCT TCAGACATGT CATTAGTTGA	360
TTAGAGGAAC AACTAGTTCT TTTTACCTAA TGCGGCGTCT TATTACATTT TTTATAATCT	420
GTAATTTATG TTTTTTTGTT GTTGTTAACA TTGGAATCTT ATAATGTTGT TGCCTGGTCT	480
TTTGTGTCTG TAATATAAGT GTCTTCAAAA GGTGTTTGC TAAATTTTCAG CAGCCTAAAA	540
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA	572

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: sre.pk0044.f3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Pro Gly Ala Leu Met Lys Phe Leu Asp Pro Phe Ser Pro Arg Trp
 1 5 10 15

Asn Ile Ser Leu Phe His Tyr Arg Gly Glu Gly Glu Thr Gly Ala Asn
20 25 30

Val Leu Val Gly Ile Gln Val Pro Lys Ser Glu Met Asp Glu Phe His
35 40 45

Asp Arg Ala Asn Lys Leu Gly Tyr Asp Tyr Lys Val Val Asn Asn Asp
50 55 60

Asp Asp Phe Gln Leu Leu Met His
65 70

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Burkholderia capacia

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Ser His Asp Tyr Leu Lys Lys Ile Leu Thr Ala Arg Val Tyr
1 5 10 15

Asp Val Ala Phe Glu Thr Glu Leu Glu Pro Ala Arg Asn Leu Ser Ala
20 25 30

Arg Leu Arg Asn Pro Val Tyr Leu Lys Arg Glu Asp Asn Gln Pro Val
35 40 45

Phe Ser Phe Lys Leu Arg Gly Ala Tyr Asn Lys Met Ala His Ile Pro
50 55 60

Ala Asp Ala Leu Ala Arg Gly Val Ile Thr Ala Ser Ala Gly Asn His
65 70 75 80

Ala Gln Gly Val Ala Phe Ser Ala Ala Arg Met Gly Val Lys Ala Val
85 90 95

Ile Val Val Pro Val Thr Thr Pro Gln Val Lys Val Asp Ala Val Arg
100 105 110

Ala His Gly Gly Pro Gly Val Glu Val Ile Gln Ala Gly Glu Ser Tyr
115 120 125

Ser Asp Ala Tyr Ala His Ala Leu Lys Val Gln Glu Glu Arg Gly Leu
130 135 140

Thr Phe Val His Pro Phe Asp Asp Pro Tyr Val Ile Ala Gly Gln Gly
145 150 155 160

Thr Ile Ala Met Glu Ile Leu Arg Gln His Gln Gly Pro Ile His Ala
165 170 175

Ile	Phe	Val	Pro	Ile	Gly	Gly	Gly	Gly	Leu	Ala	Ala	Gly	Val	Ala	Ala		
			180					185					190				
Tyr	Val	Lys	Ala	Val	Arg	Pro	Glu	Ile	Lys	Val	Ile	Gly	Val	Gln	Ala		
		195					200					205					
Glu	Asp	Ser	Cys	Ala	Met	Ala	Gln	Ser	Leu	Gln	Ala	Gly	Lys	Arg	Val		
	210					215					220						
Glu	Leu	Ala	Glu	Val	Gly	Leu	Phe	Ala	Asp	Gly	Thr	Ala	Val	Lys	Leu		
225					230					235					240		
Val	Gly	Glu	Glu	Thr	Phe	Arg	Leu	Cys	Lys	Glu	Tyr	Leu	Asp	Gly	Val		
				245					250					255			
Val	Thr	Val	Asp	Thr	Asp	Ala	Leu	Cys	Ala	Ala	Ile	Lys	Asp	Val	Phe		
			260					265					270				
Gln	Asp	Thr	Arg	Ser	Val	Leu	Glu	Pro	Ser	Gly	Ala	Leu	Ala	Val	Ala		
		275					280					285					
Gly	Ala	Lys	Leu	Tyr	Ala	Glu	Arg	Glu	Gly	Ile	Glu	Asn	Gln	Thr	Leu		
	290					295					300						
Val	Ala	Val	Thr	Ser	Gly	Ala	Asn	Met	Asn	Phe	Asp	Arg	Met	Arg	Phe		
305					310					315					320		
Val	Ala	Glu	Arg	Ala	Glu	Val	Gly	Glu	Ala	Arg	Glu	Ala	Val	Phe	Ala		
				325				330						335			
Val	Thr	Ile	Pro	Glu	Glu	Arg	Gly	Ser	Phe	Lys	Arg	Phe	Cys	Ser	Leu		
			340					345					350				
Val	Gly	Asp	Arg	Asn	Val	Thr	Glu	Phe	Asn	Tyr	Arg	Ile	Ala	Asp	Ala		
		355					360					365					
Gln	Ser	Ala	His	Ile	Phe	Val	Gly	Val	Gln	Ile	Arg	Arg	Arg	Gly	Glu		
	370					375					380						
Ser	Ala	Asp	Ile	Ala	Ala	Asn	Phe	Glu	Ser	His	Gly	Phe	Lys	Thr	Ala		
385					390					395					400		
Asp	Leu	Thr	His	Asp	Glu	Leu	Ser	Lys	Glu	His	Ile	Arg	Tyr	Met	Val		
				405					410					415			
Gly	Gly	Arg	Ser	Pro	Leu	Ala	Leu	Asp	Glu	Arg	Leu	Phe	Arg	Phe	Glu		
			420					425					430				
Phe	Pro	Glu	Arg	Pro	Gly	Ala	Leu	Met	Lys	Phe	Leu	Ser	Ser	Met	Ala		
		435					440					445					
Pro	Asp	Trp	Asn	Ile	Ser	Leu	Phe	His	Tyr	Arg	Asn	Gln	Gly	Ala	Asp		
	450					455					460						
Tyr	Ser	Ser	Ile	Leu	Val	Gly	Leu	Gln	Val	Pro	Gln	Ala	Asp	His	Ala		
465					470					475					480		
Glu	Phe	Glu	Arg	Phe	Leu	Ala	Ala	Leu	Gly	Tyr	Pro	Tyr	Val	Glu	Glu		
				485					490					495			

Ser Ala Asn Pro Ala Tyr Arg Leu Phe Leu Ser
500 505

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: cc3.mn0002d2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACGAGACGAG	TCCCCTCCCC	CCACCTCGCC	TCACCCAACC	GGAACGAACA	AGTTACCATC	60
TCATCCCAAC	CCCGCCTCGA	CCGGATCTCG	TCGGACTCGG	ATCCGCCCCG	CCACCCCGCG	120
CCGCCGCAGA	TCAAAGAAGA	TGGCAGCTCT	CGACACCTTC	CTCTTCACCT	CGGAGTCTGT	180
GAACGAGGGA	CACCCTGACA	AGCTCTGCGA	CCAGGTCTCA	GATGCCGTTC	TTGACGCTTG	240
CCTTGCTGAG	GACCCTGACA	GCAAGGTTGC	TTGTGAGACC	TGCACCAAGA	CCAACATGGT	300
CATGGTCTTT	GGTGAGATCA	CCACCAAGGC	CAATGTCGAC	TACGAGAAGA	TTGTCAGGGA	360
GACCTGCCGC	AACATTGGTT	TTGTGTCAAA	CGATGTCGGG	CTTGACGCTG	ACCACTGCAA	420
GGTGCTCGTG	AACATTGAGC	AGCAGTCCCC	TGATATTGCT	CAGGGTGTGC	ATGGCCACTT	480
CACCAAGCGC	CCCGAGGAGA	TTGGAGCTGG	TGACCAGGGA	CACATGTTTC	GGTATGCGAC	540
CGATGAGACC	CCTGAGTTGA	TGCCCCCTCAG	CCATGTCCTT	GCCACCAAGC	TAGGTGCTCG	600
TCTCACCGAG	GTCCGCAAGA	ACGGAACCTG	CCCCTGGCTC	AGGCCTGATG	GGAAGACCCA	660
GGTGACAGTC	GAGTACCGCA	ATGAGGGTGG	TGCCATGGTC	CCCATCCGTG	TCCACACCGT	720
CCTCATCTCC	ACCCAGCACG	ACGAGACAGT	GACCAATGAT	GAGATCGCTG	CTGACCTGAA	780
GGAGCATGTC	ATCAAGCCTA	TCATCCCTGA	GCAGTACCTT	GACGAGAAGA	CCATCTTCCA	840
CCTTAACCCA	TCCGGCCGCT	TTGTCATTGG	TGGACCTCAC	GGCGATGCTG	GCCTCACTGG	900
CCGCAAGATC	ATCATTGACA	CCTACGGTGG	CTGGGGAGCC	CATGGCGGTG	GCGCTTTCTC	960
CGGCAAGGAC	CCAACCAAGG	TTGACCGCAG	CGGAGCCTAT	GTCGCGAGGC	AGGCTGCCAA	1020
GAGCATCGTC	GCCAGCGGCC	TTGCTCGCCG	CGCCATCGTC	CAGGTGTCCT	ACGCCATCGG	1080
CGTGCCCGAG	CCTCTCTCCG	TGTTTGTCTG	CACGTACGGC	ACCGGCGCGA	TCCCCGACAA	1140
GGAGATCCTC	AAGATTGTCA	AGGAGAACTT	CGATTTTCAGG	CCTGGCATGA	TTATCATCAA	1200
CCTTGACCTC	AAGAAAGGCG	GCAACGGGCG	CTACCTCAAG	ACGGCAGCCT	ACGGCCACTT	1260

CGGAAGGGAC GACCCTGACT TCACCTGGGA GGTGGTGAAG CCACTCAAGT CGGAGAAACC	1320
TTCTGCCTAA GCGGGCCTTT TTTTCAGTAA GAAGCTTTTG GTGGTCTGCT GTGCTTAATC	1380
ATGCTTTTAT ATGGCTTCTA CATGTTGTGG TTCTTTCTTG ATCTGCACCG CGCTTATCGT	1440
TTGTGTTGTA CTGCCCTAAT AAGTGGTGCT TATGAGGACT GTTTCTGGTT TTGCTGCTTA	1500
TGTTGTAATG CTTTGAAACA ATGAAAGAAG CTACAGGCCA CAGCTATTTT GAGAAGTAAT	1560
GGAACCTCGT GCCGTTTTGA TT	1582

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: cc3.mn0002.d2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Ala	Ala	Leu	Asp	Thr	Phe	Leu	Phe	Thr	Ser	Glu	Ser	Val	Asn	Glu	1	5	10	15
Gly	His	Pro	Asp	Lys	Leu	Cys	Asp	Gln	Val	Ser	Asp	Ala	Val	Leu	Asp	20	25	30	
Ala	Cys	Leu	Ala	Glu	Asp	Pro	Asp	Ser	Lys	Val	Ala	Cys	Glu	Thr	Cys	35	40	45	
Thr	Lys	Thr	Asn	Met	Val	Met	Val	Phe	Gly	Glu	Ile	Thr	Thr	Lys	Ala	50	55	60	
Asn	Val	Asp	Tyr	Glu	Lys	Ile	Val	Arg	Glu	Thr	Cys	Arg	Asn	Ile	Gly	65	70	75	80
Phe	Val	Ser	Asn	Asp	Val	Gly	Leu	Asp	Ala	Asp	His	Cys	Lys	Val	Leu	85	90	95	
Val	Asn	Ile	Glu	Gln	Gln	Ser	Pro	Asp	Ile	Ala	Gln	Gly	Val	His	Gly	100	105	110	
His	Phe	Thr	Lys	Arg	Pro	Glu	Glu	Ile	Gly	Ala	Gly	Asp	Gln	Gly	His	115	120	125	
Met	Phe	Gly	Tyr	Ala	Thr	Asp	Glu	Thr	Pro	Glu	Leu	Met	Pro	Leu	Ser	130	135	140	
His	Val	Leu	Ala	Thr	Lys	Leu	Gly	Ala	Arg	Leu	Thr	Glu	Val	Arg	Lys	145	150	155	160
Asn	Gly	Thr	Cys	Pro	Trp	Leu	Arg	Pro	Asp	Gly	Lys	Thr	Gln	Val	Thr	165	170	175	

Val Glu Tyr Arg Asn Glu Gly Gly Ala Met Val Pro Ile Arg Val His
 180 185 190
 Thr Val Leu Ile Ser Thr Gln His Asp Glu Thr Val Thr Asn Asp Glu
 195 200 205
 Ile Ala Ala Asp Leu Lys Glu His Val Ile Lys Pro Ile Ile Pro Glu
 210 215 220
 Gln Tyr Leu Asp Glu Lys Thr Ile Phe His Leu Asn Pro Ser Gly Arg
 225 230 235 240
 Phe Val Ile Gly Gly Pro His Gly Asp Ala Gly Leu Thr Gly Arg Lys
 245 250 255
 Ile Ile Ile Asp Thr Tyr Gly Gly Trp Gly Ala His Gly Gly Gly Ala
 260 265 270
 Phe Ser Gly Lys Asp Pro Thr Lys Val Asp Arg Ser Gly Ala Tyr Val
 275 280 285
 Ala Arg Gln Ala Ala Lys Ser Ile Val Ala Ser Gly Leu Ala Arg Arg
 290 295 300
 Ala Ile Val Gln Val Ser Tyr Ala Ile Gly Val Pro Glu Pro Leu Ser
 305 310 315 320
 Val Phe Val Asp Thr Tyr Gly Thr Gly Ala Ile Pro Asp Lys Glu Ile
 325 330 335
 Leu Lys Ile Val Lys Glu Asn Phe Asp Phe Arg Pro Gly Met Ile Ile
 340 345 350
 Ile Asn Leu Asp Leu Lys Lys Gly Gly Asn Gly Arg Tyr Leu Lys Thr
 355 360 365
 Ala Ala Tyr Gly His Phe Gly Arg Asp Asp Pro Asp Phe Thr Trp Glu
 370 375 380
 Val Val Lys Pro Leu Lys Ser Glu Lys Pro Ser Ala
 385 390 395

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2183 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Oryza sativa

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCTTAT AAATGAACGG AAAATGGAAA AAAAAATTGA TTGGTGCCAC TTCAAAGTTA 60
 AATATGCCAA GACGAATTGA TATGTTTCTG CTGTTGTTTT ATGCTCTTGA TTAGTTGATG 120

CGCATGTTCA	ATGATTTATG	ATGTTTGTCT	TTGTGGAAAG	ATTACATGTA	AAGAGTATAG	180
TAGAACCCCT	AAAAGCTAGC	CAGCGATTTC	GCTCTTTTTT	TCCAGGTCTC	CATGATATGT	240
TTACCCCTAA	AAGTGGTATA	TTTATGTGAT	AGTTACAATA	CATAGTGGAC	CACGATTGAT	300
TATGCGTTTA	TGCTGATTCC	GGCAGAAAAT	TGTTAGATTG	CTTGTGCTCT	ATACCTGCTT	360
GTTGCGCTTG	TAGAGAATAT	TACAAATACC	TAACACTTGC	CCAAGGAACT	TAGGAACTTA	420
GTCAACTCTT	TGTAGGGACA	ACTATTTTAG	CCCAAATTG	TGGTCTTGTC	AGGTGCCAAC	480
AAAACAGCAT	CTTGGCGTAC	ATAAGCTATA	TAGAGGATTA	AAAGGAATGT	TTTGTTCCTT	540
GCTACTGTTT	TTTTAACCTG	TTTACTCAGG	ACAAATTTTG	TTGCATAAAC	CATTTGTTCT	600
AGGGATCAGT	ATTGTCCTCT	CAGTGTGTTA	TGTAAGCATT	TCCAGAAATC	AATTGTCGCT	660
ATCAGCTTCC	CTCACATTAG	CTATCACTTA	TACCCCTTTT	TTTCTCATAG	GCTCACCATG	720
TCCATTTTAT	TCATGATATT	TCTTTGTCTA	AAGTATGTGA	AATACCATTT	TATGCAGATA	780
GGAGAAGATG	GCCGCACTTG	ATACCTTCCT	CTTTACCTCG	GAGTCTGTGA	ACGAGGGCCA	840
CCCTGACAAG	CTCTGCGACC	AAGTCTCAGA	TGCTGTGCTT	GATGCCTGCC	TCGCCGAGGA	900
CCCTGACAGC	AAGGTCGCTT	GTGAGACCTG	CACCAAGACA	AACATGGTCA	TGGTCTTTGG	960
TGAGATCACC	ACCAAGGCTA	ACGTTGACTA	TGAGAAGATT	GTCAGGGAGA	CATGCCGTAA	1020
CATCGGTTTT	GTGTCAGCTG	ATGTCGGTCT	CGATGCTGAC	CACTGCAAGG	TGCTTGTGAA	1080
CATCGAGCAG	CAGTCCCCTG	ACATTGCACA	GGGTGTGCAC	GGGCACTTCA	CCAAGCGCCC	1140
TGAGGAGATT	GGTGCTGGTG	ACCAGGGACA	CATGTTTGGA	TATGCAACTG	ATGAGACCCC	1200
TGAGTTGATG	CCCCTCAGCC	ATGTCCTTGC	TACCAAGCTT	GGCGCTCGTC	TTACGGAGGT	1260
TCGCAAGAAT	GGGACCTGCG	CATGGCTCAG	GCCTGACGGG	AAGACCCAAG	TGACTGTTGA	1320
GTACCGCAAT	GAGAGCGGTG	CCAGGGTCCC	TGTCCGTGTC	CACACCGTCC	TCATCTCTAC	1380
CCAGCATGAT	GAGACAGTCA	CCAACGATGA	GATTGCTGCT	GACCTGAAGG	AGCATGTCAT	1440
CAAGCCTGTC	ATCCCGAGC	AGTACCTTGA	TGAGAAGACA	ATCTTCCATC	TTAACCCTATC	1500
TGGTCGCTTC	GTCATTGGCG	GACCTCATGG	TGATGCTGGT	CTCACTGGCC	GGAAGATCAT	1560
CATTGACACT	TATGGTGGCT	GGGGAGCTCA	CGGTGGTGGT	GCCTTCTCTG	GCAAGGACCC	1620
AACCAAGGTT	GACCGCAGTG	GAGCATACGT	CGCAAGGCAA	GCTGCCAAGA	GCATTGTTGC	1680
TAGTGGCCTT	GCTCGCCGCT	GCATTGTCCA	AGTATCATAC	GCCATCGGTG	TCCCAGAGCC	1740
ACTGTCCGTA	TTCGTCGACA	CATACGGCAC	TGGCAGGATC	CCTGACAAGG	AGATCCTCAA	1800
GATTGTGAAG	GAGAACTTCG	ACTTCAGGCC	TGGCATGATC	ATCATCAACC	TTGACCTCAA	1860
GAAAGGCGGC	AACGGACGCT	ACCTCAAGAC	GGCGGCTTAC	GGTCACTTCG	GAAGGGACGA	1920

CCCAGACTTC ACCTGGGAGG TGGTGAAGCC CCTCAAGTGG GAGAAGCCTT CTGCCTAAAA	1980
GCTCCCTTTC GGAGGCTTTT GCTCTGTCCC ATTATGGTGT TTTGTTTCCT CGCTGCTCAG	2040
CATTGTGATT CTTAACCTGC CCCCCGCTGC CATTTATGCC CATGCACGCT ACTTTCCTAA	2100
TAATAAGTAC TTATAAGGGT ATTGTGTTTG AATATTTTAC CTAGAGGAGG AGGAGGATTT	2160
GTTATCTGTT ATTGCTTAAG CTT	2183

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: s2.12b06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGCCAAGCCC CACTCAACCA CCACACCACT CTCTCTGCTC TTCTTCTACC TTTCAAGTTT	60
TTAAAGTATT AAGATGGCAG AGACATTCCT ATTTACCTCA GAGTCAGTGA ACGAGGGACA	120
CCCTGACAAG CTCTGCGACC AAATCTCCGA TGCTGTCCTC GACGCTTGCC TTGAACAGGA	180
CCCAGACAGC AAGGTTGCCT GCGAAACATG CACCAAGACC AACTTGGTCA TGGTCTTCGG	240
AGAGATCACC ACCAAGGCCA ACGTTGACTA CGAGAAGATC GTGCGTGACA CCTGCAGGAA	300
CATCGGCTTC GTCTCAAACG ATGTGGGACT TGATGCTGAC AACTGCAAGG TCCTTGTA	360
CATTGAGCAG CAGAGCCCTG ATATTGCCCA GGGTGTGCAC GGCCACCTTA CCAAAAGACC	420
CGAGGAAATC GGTGCTGGAG ACCAGGGTCA CATGTTTGGC TATGCCACGG ACGAAACCCC	480
AGAATTGATG CCATTGAGTC ATGTTCTTGC AACTAAACTC GGTGCTCGTC TCACCGAGGT	540
TCGCAAGAAC GGAACCTGCC CATGGTTGAG GCCTGATGGG AAAACCCAAG TGA	600
GTATTACAAT GACAACGGTG CCATGGTTCC AGTTCGTGTC CACACTGTGC TTATCTCCAC	660
CCAACATGAT GAGACTGTGA CCAACGACGA AATTGCAGCT GACCTCAAGG AGCATGTGAT	720
CAAGCCGGTG ATCCCGGAGA AGTACCTTGA TGAGAAGACC ATTTTCCACT TGAACCCCTC	780
TGGCCGTTTT GTCATTGGAG GTCCTCACGG TGATGCTGGT CTCACCGGCC GCAAGATCAT	840
CATCGATACT TACGGAGGAT GGGGTGCTCA TGGTGGTGGT GCTTTCTCCG GGAAGGATCC	900
CACCAAGGTT GATAGGAGTG GTGCTTACAT TGTGAGACAG GCTGCTAAGA GCATTGTGGC	960
AAGTGGACTA GCCAGAAGGT GCATTGTGCA AGTGTCTTAT GCCATTGGTG TGCCCGAGCC	1020

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TTTGTCTGTC TTTGTTGACA CCTATGGCAC CGGGAAGATC CATGATAAGG AGATTCTCAA      1080
CATTGTGAAG GAGAACTTTG ATTTTCAGGCC CGGTATGATC TCCATCAACC TTGATCTCAA      1140
GAGGGGTGGG AATAACAGGT TCTTGAAGAC TGCTGCATAT GGACACTTCG GCAGAGAGGA      1200
CCCTGACTTC ACATGGGAAG TGGTCAAGCC CCTCAAGTGG GAGAAGGCCT AAGGCCATTC      1260
ATTCCACTGC AATGTGCTGG GAGTTTTTTTA GCGTTGCCCT TATAATGTCT ATTATCCATA      1320
ACTTTCCACG TCCCTTGCTC TGTGTTTTTC TCTCGTCGTC CTCCTCCTAT TTTGTTTCTC      1380
CTGCCTTTCA TTTGTAATTT TTTACATGAT CAACTAAAAA ATGTACTCTC TGTTTTCCGA      1440
CCATTGTGTC TCTTAATATC AGTATCAAAA AGAATGTTCC AAGTT                        1485

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(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 392 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: s2.12b06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

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Met Ala Glu Thr Phe Leu Phe Thr Ser Glu Ser Val Asn Glu Gly His
1           5           10           15
Pro Asp Lys Leu Cys Asp Gln Ile Ser Asp Ala Val Leu Asp Ala Cys
20          25          30
Leu Glu Gln Asp Pro Asp Ser Lys Val Ala Cys Glu Thr Cys Thr Lys
35          40          45
Thr Asn Leu Val Met Val Phe Gly Glu Ile Thr Thr Lys Ala Asn Val
50          55          60
Asp Tyr Glu Lys Ile Val Arg Asp Thr Cys Arg Asn Ile Gly Phe Val
65          70          75          80
Ser Asn Asp Val Gly Leu Asp Ala Asp Asn Cys Lys Val Leu Val Asn
85          90          95
Ile Glu Gln Gln Ser Pro Asp Ile Ala Gln Gly Val His Gly His Leu
100         105         110
Thr Lys Arg Pro Glu Glu Ile Gly Ala Gly Asp Gln Gly His Met Phe
115        120        125
Gly Tyr Ala Thr Asp Glu Thr Pro Glu Leu Met Pro Leu Ser His Val
130        135        140
Leu Ala Thr Lys Leu Gly Ala Arg Leu Thr Glu Val Arg Lys Asn Gly
145        150        155        160

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Thr Cys Pro Trp Leu Arg Pro Asp Gly Lys Thr Gln Val Thr Val Glu
 165 170 175
 Tyr Tyr Asn Asp Asn Gly Ala Met Val Pro Val Arg Val His Thr Val
 180 185 190
 Leu Ile Ser Thr Gln His Asp Glu Thr Val Thr Asn Asp Glu Ile Ala
 195 200 205
 Ala Asp Leu Lys Glu His Val Ile Lys Pro Val Ile Pro Glu Lys, Tyr
 210 215 220
 Leu Asp Glu Lys Thr Ile Phe His Leu Asn Pro Ser Gly Arg Phe Val
 225 230 235 240
 Ile Gly Gly Pro His Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile
 245 250 255
 Ile Asp Thr Tyr Gly Gly Trp Gly Ala His Gly Gly Gly Ala Phe Ser
 260 265 270
 Gly Lys Asp Pro Thr Lys Val Asp Arg Ser Gly Ala Tyr Ile Val Arg
 275 280 285
 Gln Ala Ala Lys Ser Ile Val Ala Ser Gly Leu Ala Arg Arg Cys Ile
 290 295 300
 Val Gln Val Ser Tyr Ala Ile Gly Val Pro Glu Pro Leu Ser Val Phe
 305 310 315 320
 Val Asp Thr Tyr Gly Thr Gly Lys Ile His Asp Lys Glu Ile Leu Asn
 325 330 335
 Ile Val Lys Glu Asn Phe Asp Phe Arg Pro Gly Met Ile Ser Ile Asn
 340 345 350
 Leu Asp Leu Lys Arg Gly Gly Asn Asn Arg Phe Leu Lys Thr Ala Ala
 355 360 365
 Tyr Gly His Phe Gly Arg Glu Asp Pro Asp Phe Thr Trp Glu Val Val
 370 375 380
 Lys Pro Leu Lys Trp Glu Lys Ala
 385 390

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAATTCCTAC AAAGAGGTTA TTTCTCTCAA GGGGTAAAAA GATTGCCCCT TTTGACATT	60
TATAATCCTC TTTTCTCTT TGTTGCGCGT TGGGTTCTTC ACTTTCCTGT TTCTTGAGAA	120
TGGAAACTTT CTTATTCACC TCCGAGTCTG TGAACGAGGG TCACCCAGAC AAGCTCTGTG	180
ATCAGATCTC TGATGCAGTT CTTGATGCCT GCCTTGAGCA AGATCCCGAG AGCAAAGTTG	240
CATGTGAAAC TTGCACCAAG ACCAACTTGG TCATGGTCTT TGGTGAGATC ACAACCAAGG	300
CTATTGTAGA CTATGAGAAG ATTGTGCGTG ACACATGCCG TAATATTGGA TTTGTTTCTG	360
ATGATGTTGG TCTTGATGCT GACAACTGCA AGGTCCTTGT TTACATTGAG CAGCAAAGTC	420
CTGATATTGC TCAAGGTGTC CACGGCCATC TGACCAAACG CCCCAGGAG ATTGGTGCTG	480
GTGACCAGGG CCACATGTTT GGCTATGCAA CAGATGAGAC CCCTGAATTA ATGCCTCTCA	540
GTCACGTGCT TGCAACTAAA CTTGGTGCCC GTCTTACAGA AGTCCGCAAG AATGGCACCT	600
GCGCCTGGTT GAGGCCTGAT GGCAAGACCC AAGTTACTGT TGAGTATAGC AATGACAATG	660
GTGCCATGGT TCCAATTAGG GTACACACTG TTCTTATCTC CACCCAACAC GATGAGACCG	720
TTACCAATGA TGAGATTGCC CGCGACCTTA AGGAGCATGT CATCAAACCA GTCATCCCAG	780
AGAAGTACCT TGATGAGAAT ACTATTTTCC ACCTTAACCC ATCTGGCCGA TTCGTTATTG	840
GTGGACCTCA TGGTGATGCT GGTCTCACTG GTCGTAAAAT CATCATCGAC ACTTATGGTG	900
GTTGGGGTGC TCATGGTGGT GGTGCTTTCT CGGGCAAAGA CCCAACCAAG GTCGACAGGA	960
GTGGTGCATA CATTGTAAGG CAGGCTGCAA AGAGTATCGT AGCTAGTGGA CTTGCTCGTA	1020
GATGCATCGT GCAGGTATCT TATGCCATCG GTGTGCCTGA GCCATTGTCT GTATTTCGTTG	1080
ACACCTATGG CACTGGAAAG ATCCCTGACA GGGAAATTTT GAAGATCGTT AAGGAGAACT	1140
TTGACTTCAG ACCTGGAATG ATGTCCATTA ACTTGGATTT GAAGAGGGGT GGCAATAGAA	1200
GATTCTTGAA AACTGCTGCC TATGGTCACT TTGGACGTGA TGACCCCGAT TTCACATGGG	1260
AAGTTGTCAA GCCCCTCAAG TGGGAAAAGC CCCAAGACTA ATAAGTGCTT GCCTATGTTT	1320
TTGTTCTTTG TTGTTTGCTT GTGGCTTTAG AATCTCCCC GTGTTTGCTT GTTTGTCTTT	1380
GTATTTTCTC TTTTGACCCT TTATTTTGTT ATTGTCCTGT TTCCATTGTG TTGGATGGAT	1440
ATCTTAGGCC TTGGAATATT AAGGAAAGAA AAGGAATTC	1479

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCTCCCTTC	GGTTCATCGG	CCTCCCGATC	GAGCAGTAGA	AGCAGCGCAA	GGGCATCGCT	60
AGCACTAAAG	AAATGGCAGC	CGAGACGTTC	CTCTTCACGT	CCGAGTCTGT	GAACGAGGGC	120
CATCCCGACA	AGCTCTGTGA	CCAAGTCTCC	GACGCCGTCT	TGGATGCCTG	CTTGGCCCAG	180
GATGCCGACA	GCAAGGTCGC	CTGCGAGACC	GTCACCAAGA	CCAACATGGT	CATGGTCTTG	240
GGCGAGATCA	CCACCAAGGC	CACCGTCGAC	TATGAGAAGA	TCGTGCGTGA	CACCTGCCGC	300
AACATCGGTT	TCATCTCTGA	TGACGTTGGT	CTCGACGCCG	ACCGTTGCAA	RGTGCTCGTC	360
AACATCGAGC	AGCAGTCCCC	TGACATTGCC	CAGGGTGTTT	ATGGACACTT	CACCAAGCGT	420
CCCGAAGAAG	TCGGCGCCGG	TGACCAGGGC	ATCATGTTTC	GCTATGCCAC	CGATGAGACC	480
CCTGAGCTGA	TGCCCCCTCA	GCACGTGCTT	GCCACCAAGC	TYGGAGCTCG	CCTCACSGAG	540
GTCCGCAAGA	ATGGCACCTG	CGCCTGGGTC	AGGCCTGACG	GAAAGACCCA	GGTCACAGTC	600
GAGTACCTAA	ACGAGGATGG	TGCCATGGTA	CCTGTTCGTG	TGCACACCGT	CCTCATCTCC	660
ACCCAGCACG	ACGAGACCGT	CACCAACGAC	GAGATTGCTG	CGGACCTCAA	GGAGCATGTC	720
ATCAAGCCGG	TGATCCCCGC	AAAGTACCTC	GATGAGAACA	CCATCTTCCA	CCTGAACCCG	780
TCTGGCCGCT	TCGTATCGGG	CGGCCCCCAC	GGTGACGCCG	GTCTCACC GG	CCGCAAGATC	840
ATCATCGACA	CCTATGGTGG	CTGGGGAGCC	CACGGCGGCG	GTGCCTTCTC	TGGCAAGGAC	900
CCAACCAAGG	TCGACCGYAG	TGGCGCCTAC	ATTGCCAGGC	ARGCCGCCAA	GAGCATCATC	960
GCCAGCGGCC	TCGCACGCCG	CTGCATTGTG	CAGATCTCAT	ACGCCATCGG	TGTGCCTGAG	1020
CCTTTGTCTG	TGTTTCGTGA	CTCCTACGGC	ACCGGCAAGA	TCCCCGACAG	GGAGATCCTC	1080
AAGCTCGTGA	AGGAGAACTT	TGACTTCAGG	CCCGGGATGA	TCAGCATCAA	CCTGGACTTG	1140
AAGAAAGGTG	GAAACAGGTT	CATCAAGACC	GCTGCTTACG	GTCACCTTTG	CCGTGATGAT	1200
GCCGACTTCA	CCTGGGAGGT	GGTGAAGCCC	CTCAAGTTTC	ACAAGGCATC	TGCCTAAGAG	1260
CATGGCATTC	TCTTGGTCTG	CCGCCTCTCA	AGTTCGTCAA	GACGGGATCA	TGTTGCTCCT	1320
GGGAAGTGGG	AAGAAGCATT	AGACATTGAA	GCGACGCTCT	ACACTGGTCT	TGTTGTATGG	1380

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Ala	Ala	Glu	Thr	Phe	Leu	Phe	Thr	Ser	Glu	Ser	Val	Asn	Glu	Gly	
1				5					10					15		
His	Pro	Asp	Lys	Leu	Cys	Asp	Gln	Val	Ser	Asp	Ala	Val	Leu	Asp	Ala	
			20					25					30			
Cys	Leu	Ala	Gln	Asp	Ala	Asp	Ser	Lys	Val	Ala	Cys	Glu	Thr	Val	Thr	
		35					40					45				
Lys	Thr	Asn	Met	Val	Met	Val	Leu	Gly	Glu	Ile	Thr	Thr	Lys	Ala	Thr	
	50					55					60					
Val	Asp	Tyr	Glu	Lys	Ile	Val	Arg	Asp	Thr	Cys	Arg	Asn	Ile	Gly	Phe	
65					70					75					80	
Ile	Ser	Asp	Asp	Val	Gly	Leu	Asp	Ala	Asp	Arg	Cys	Lys	Val	Leu	Val	
				85					90					95		
Asn	Ile	Glu	Gln	Gln	Ser	Pro	Asp	Ile	Ala	Gln	Gly	Val	His	Gly	His	
			100					105					110			
Phe	Thr	Lys	Arg	Pro	Glu	Glu	Val	Gly	Ala	Gly	Asp	Gln	Gly	Ile	Met	
		115					120					125				
Phe	Gly	Tyr	Ala	Thr	Asp	Glu	Thr	Pro	Glu	Leu	Met	Pro	Leu	Lys	His	
	130					135					140					
Val	Leu	Ala	Thr	Lys	Leu	Gly	Ala	Arg	Leu	Thr	Glu	Val	Arg	Lys	Asn	
145					150					155					160	
Gly	Thr	Cys	Ala	Trp	Val	Arg	Pro	Asp	Gly	Lys	Thr	Gln	Val	Thr	Val	
				165					170					175		
Glu	Tyr	Leu	Asn	Glu	Asp	Gly	Ala	Met	Val	Pro	Val	Arg	Val	His	Thr	
			180					185						190		
Val	Leu	Ile	Ser	Thr	Gln	His	Asp	Glu	Thr	Val	Thr	Asn	Asp	Glu	Ile	
		195					200					205				
Ala	Ala	Asp	Leu	Lys	Glu	His	Val	Ile	Lys	Pro	Val	Ile	Pro	Ala	Lys	
	210					215					220					
Tyr	Leu	Asp	Glu	Asn	Thr	Ile	Phe	His	Leu	Asn	Pro	Ser	Gly	Arg	Phe	
225					230					235					240	
Val	Ile	Gly	Gly	Pro	His	Gly	Asp	Ala	Gly	Leu	Thr	Gly	Arg	Lys	Ile	
				245					250					255		
Ile	Ile	Asp	Thr	Tyr	Gly	Gly	Trp	Gly	Ala	His	Gly	Gly	Gly	Ala	Phe	
			260					265					270			
Ser	Gly	Lys	Asp	Pro	Thr	Lys	Val	Asp	Arg	Ser	Gly	Ala	Tyr	Ile	Ala	
		275					280					285				
Arg	Gln	Ala	Ala	Lys	Ser	Ile	Ile	Ala	Ser	Gly	Leu	Ala	Arg	Arg	Cys	
	290					295					300					
Ile	Val	Gln	Ile	Ser	Tyr	Ala	Ile	Gly	Val	Pro	Glu	Pro	Leu	Ser	Val	
305					310					315					320	

AGTGGCGCCT	ACATTGCCAG	GCAGGCTGCC	AAGAGCATCA	TCGCCAGCGG	CCTCGCACGC	960
CGGTGCATTG	TGCAGATCTC	ATATGCCATC	GGTGTACCTG	AGCCTTTGTC	TGTGTTTCGTC	1020
GACTCCTACG	GCACTGGCAA	GATCCCTGAC	AGGGAGATCC	TCAAGCTCGT	GAAGGAGAAC	1080
TTTGACTIONCA	GACCCGGGAT	GATCACGATC	AACCTCGACT	TGAAGAAAGG	TGGAAACAGG	1140
TTCATCAAGA	CAGCTGCTTA	CGGTCACTTT	GGCCGCGATG	ATGCTGACTT	CACCTGGGAG	1200
GTGGTGAAGC	CCCTCAAGTT	CGACAAGGCA	TCTGCTTAAG	AAGAAGACAT	CACATTGAGG	1260
GTTCTTCTTG	GTCTGATGCC	TCTCAAGTTC	GGCAAGGCGG	GATCCTTTTG	CTCCTCGGAA	1320
GTAAGAAGAA	GCATTCAACA	TCGCCCCGAA	TTC			1353